

Gencore version 5.1.4_P5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:07:15 ; Search time 991 seconds
 (without alignments)
 293,671 Million cell updates/sec

Title: US-09-702-498a-33-MOD
 Perfect score: 10
 Sequence: 1 CuuuCACCCu 10

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenBank:*

1: gb_bat:*

2: gb_hhg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sis:*

12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_patt:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_v1:*

29: em_v1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rod:*

36: em_htg_man:*

37: em_htg_vct:*

38: em_jy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	6 AX134713	AX134713 Sequence
2	10	100.0	10	6 AX177327	AX477327 Sequence
3	10	100.0	11	6 118631	118631 Sequence 1
4	10	100.0	12	6 AR030044	AR030044 Sequence
5	10	100.0	19	6 AR099568	AR099568 Sequence
6	10	100.0	19	6 AR178849	AR178849 Sequence
7	10	100.0	21	6 AX108449	AX108449 Sequence
8	10	100.0	21	6 AX108450	AX108450 Sequence
9	10	100.0	21	6 AX17439	AX17439 Sequence
10	10	100.0	21	6 AX176918	AX176918 Sequence
11	10	100.0	21	6 BD013048	BD013048 Paramykov
12	10	100.0	21	6 BD013049	BD013049 Paramykov
13	10	100.0	21	6 BD010081	Bd010081 Paramykov
14	10	100.0	21	6 BD010082	Bd010082 Paramykov
15	10	100.0	22	6 AR099567	AR099567 Sequence
16	10	100.0	22	6 AR178848	AR178848 Sequence
17	10	100.0	23	6 AR011697	AR011697 Sequence
18	10	100.0	23	6 AR09297	AR09297 Sequence
19	10	100.0	23	6 AR119514	AR119514 Sequence
20	10	100.0	23	6 AR122431	AR122431 Sequence
21	10	100.0	23	6 I33071	I33071 Sequence 7
22	10	100.0	24	6 AR099566	AR099566 Sequence
23	10	100.0	24	6 AR178847	AR178847 Sequence
24	10	100.0	47	6 BD011795	BD011795 RNP deriv
25	10	100.0	47	6 BD011797	BD011797 RNP deriv
26	10	100.0	47	6 BD004193	Bd004193 RNP deriv
27	10	100.0	47	6 BD004194	Bd004194 RNP deriv
28	10	100.0	53	6 A78690	A78690 Sequence 7
29	10	100.0	58	1 AF195107	AF195107 Sulfolobu
30	10	100.0	58	6 E47180	E47180 Process for
31	10	100.0	64	6 BD013043	BD013043 Paramykov
32	10	100.0	64	6 BD010076	Bd010076 Paramykov
33	10	100.0	72	6 BD011787	BD011787 RNP deriv
34	10	100.0	72	6 BD011804	BD011804 RNP deriv
35	10	100.0	72	6 BD011805	BD011805 RNP deriv
36	10	100.0	72	6 BD004184	Bd004184 RNP deriv
37	10	100.0	72	6 BD004201	Bd004201 RNP deriv
38	10	100.0	72	6 BD004202	Bd004202 RNP deriv
39	10	100.0	74	6 BD011784	BD011784 RNP deriv
40	10	100.0	74	6 BD011785	BD011785 RNP deriv
41	10	100.0	74	6 BD004181	Bd004181 RNP deriv
42	10	100.0	74	6 BD004182	Bd004182 RNP deriv
43	10	100.0	76	6 AX134717	AX134717 Sequence
44	10	100.0	80	6 BD011771	BD011771 RNP deriv
45	10	100.0	80	6 BD004168	Bd004168 RNP deriv

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

RESULT 1
 AX134713
 LOCUS AX134713
 DEFINITION Sequence 1 from Patent WO0132898.
 ACCESSION AX134713
 VERSION AX134713.1 GI:14271230
 KEYWORDS SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 1 (bases 1 to 10)
 AUTHORS Yonemitsu, Y., Hasagawa, M. and Alton, E.
 TITLE Recombinant Sendai virus vector for introducing exogenous genes to
 airway epithelia
 Patent: WO 0132898-A 1 10-MAY-2001;
 JOURNAL

FEATURES source Dnavec Research Inc. (JP) Location/qualifiers

1. .10 /organism="synthetic construct" /db_xref="taxon:32630" /note="artificially synthesized sequence"

BASE COUNT 1 a 5 c 0 g 4 t

ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 10; Best Local Similarity 60.0%; Pred. No. 2.1e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; /note="Artificially synthesized sequence"

QY 1 CUUCACCCU 10

Db 1 CTTTACCCCT 10

RESULT 2

AX477327

LOCUS AX477327 Sequence 1 from Patent WO0238726. 10 bp DNA linear PAT 12-AUG-2002

DEFINITION AX477327

ACCESSION AX477327.1 GI:22216577

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Griesenbach, U., Ferrari, S., Geddes, D.M., Alton, E.W., Hasegawa, M.

TITLE Paramyxovirus vector for gene transfer to the cardiovascular system

JOURNAL Patent: WO 0238726-A 1 16-MAY-2002;

Dnavec Research Inc. (JP)

FEATURES

source

1. .10

/organism="synthetic construct" /db_xref="taxon:32630" /note="Artificially Synthesized Sequence"

BASE COUNT 1 a 5 c 0 g 4 t

ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 10; Best Local Similarity 60.0%; Pred. No. 2.1e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; /note="Artificially Synthesized Sequence"

QY 1 CUUCACCCU 10

Db 1 CTTTACCCCT 10

RESULT 3

1I8631/c

LOCUS 1I8631 Sequence 1 from Patent US 5500343. 11 bp DNA linear PAT 07-OCT-1996

DEFINITION 1I8631.1 GI:1598986

ACCESSION 1I8631

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Blum, K., Noble, E.P. and Sheridan, P.J.

TITLE Allelic association of the human dopamine(D2) receptor gene in compulsive disorders

JOURNAL Patent: US 5500343-A 1 19-MAR-1996;

FEATURES

source

1. .11

/organism="unknown" /note="Unknown"

BASE COUNT 4 a 0 c 6 g 1 t

ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 11; Best Local Similarity 60.0%; Pred. No. 1.9e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; /note="Unknown"

QY 1 CUUCACCCU 10

Db 7 CTTTACCCCT 16

RESULT 4

AR030044/c

LOCUS AR030044 Sequence 233 from Patent US 5861244. 12 bp DNA linear PAT 29-SEP-1999

DEFINITION AR030044

ACCESSION AR030044

VERSION AR030044.1 GI:5943258

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Wang, C.-G. and Hepburn, A.G.

TITLE Genetic sequence assay using DNA triple strand formation

JOURNAL Patent: US 5861244-A 233 19-JAN-1999;

FEATURES

source

1. .12

/organism="unknown"

BASE COUNT 5 a 0 c 6 g 1 t

ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 12; Best Local Similarity 60.0%; Pred. No. 2.1e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; /organism="unknown"

QY 1 CUUCACCCU 10

Db 12 CTTTACCCCT 3

RESULT 5

AR099568

LOCUS AR099568 Sequence 95 from patent US 6077833. 19 bp DNA linear PAT 14-FEB-2001

DEFINITION AR099568

ACCESSION AR099568

VERSION AR099568.1 GI:12809334

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS Bennett, C. Frank, and Vickers, T.A.

TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein

JOURNAL Patent: US 6077833-A 5 20-JUN-2000;

FEATURES

source

1. .19

/organism="unknown"

BASE COUNT 4 a 6 c 4 g 5 t

ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 19; Best Local Similarity 60.0%; Pred. No. 1.9e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; /organism="unknown"

QY 1 CUUCACCCU 10

Db 7 CTTTACCCCT 16

RESULT 6

AR178849

LOCUS AR178849 Sequence 95 from patent US 6319906. 19 bp DNA linear PAT 20-APR-2002

DEFINITION AR178849

ACCESSION AR178849

VERSION AR178849.1 GI:20219987

Query Match 100.0%; Score 10; DB 6; Length 11;

KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
Unclassified.									
1 (bases 1 to 19)									
AUTHORS	Bennett,C.Frank, and Vickers,T.A.								
TITLE	Oligonucleotide compositions and methods for the modulation of the expression of B7 protein								
JOURNAL	Patent: US 6319906-A 95-20-NOV-2001;								
FEATURES	Location/Qualifiers								
source	1..19								
BASE COUNT	4	a	6	c	4	g	5	t	
ORIGIN									
Query Match	100.0%		Score 10;	DB 6;	Length 19;				
Best Local Similarity	60.0%		Pred. No. 1.9e+05;						
Matches	6;	Conservative	4;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	cuuucacccu	10						
Db	7		11						
RESULT 7	AX108449/c								
LOCUS	AX108449		21 bp	DNA	linear	PAT 30-APR-2001			
DEFINITION	Sequence 12 from Patent WO0123548.								
ACCESSION	AX108449								
VERSION	AX108449.1		GT:13943775						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	DNA-cleaving nuclease P1 rna.								
PATENT	Patent: WO 0123548-A 12-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 8	/organism="synthetic construct"								
LOCUS	/db_xref="taxon:32630"								
DEFINITION	/note="Primer"								
ACCESSION									
VERSION									
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	Dorit,R.L. and Cole,K.B.								
TITLE	DNA-cleaving nuclease P1 rna								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 9	/organism="synthetic construct"								
LOCUS	AX117439/c								
DEFINITION	Sequence 21 from Patent EP1197495.								
ACCESSION	AX117439								
VERSION	AX117439.1		GT:21522724						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Sumitomo Chemical Company, Limited (JP)								
JOURNAL	Sumitomo Chemical Company, Limited (JP)								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 10	/organism="synthetic construct"								
LOCUS	AX176918								
DEFINITION	Sequence 21 from Patent EP1197495.								
ACCESSION	AX176918								
VERSION	AX176918.1		GT:22167171						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P., Luisi,A.J., Ohman,J., Ross,D., Tafuri,S. and Wu,C.								
JOURNAL	Gene and sequence variation associated with cancer								
FEATURES	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)								
source	Location/Qualifiers								
RESULT 11	/organism="synthetic construct"								
LOCUS	AX117439								
DEFINITION	Sequence 21 from Patent EP1197495.								
ACCESSION	AX117439								
VERSION	AX117439.1		GT:21522724						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 12	/organism="synthetic construct"								
LOCUS	AX1208450								
DEFINITION	Sequence 13 from Patent WO0123548.								
ACCESSION	AX1208450								
VERSION	AX1208450.1		GT:13223776						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 13	/organism="synthetic construct"								
LOCUS	AX1208450								
DEFINITION	Sequence 13 from Patent WO0123548.								
ACCESSION	AX1208450								
VERSION	AX1208450.1		GT:13223776						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 14	/organism="synthetic construct"								
LOCUS	AX1208450								
DEFINITION	Sequence 14 from Patent WO0123548.								
ACCESSION	AX1208450								
VERSION	AX1208450.1		GT:13223776						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 15	/organism="synthetic construct"								
LOCUS	AX1208450								
DEFINITION	Sequence 15 from Patent WO0123548.								
ACCESSION	AX1208450								
VERSION	AX1208450.1		GT:13223776						
KEYWORDS									
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	artificial sequences.								
AUTHORS	1 (bases 1 to 21)								
TITLE	Dorit,R.L. and Cole,K.B.								
JOURNAL	Patent: WO 0123548-A 13-05-APR-2001;								
FEATURES	Location/Qualifiers								
source	1..21								
RESULT 16	/organism="synthetic construct"								
LOCUS	AX1208450								
DEFINITION	Sequence 16 from Patent WO0123								

Db 13 CTTTCACCC 4

RESULT 14

ID BD010082 standard; DNA; SYN; 21 BP.

XX BD010082;

XX BD010082.1

XX 08-FEB-2002 (Rel. 70, Created)

XX 08-FEB-2002 (Rel. 70, Last updated, Version 1)

DE Paramyxovirus having modified transcription initiation sequence.

KW JP 03075813-T/12.

XX OS synthetic construct.

OC artificial sequence.

XX [1]

RN 1-21

RA Nagai Y., Kato A., Hasegawa M.;

RT "Paramyxovirus having modified transcription initiation sequence";

RL Patent number JP03075813-T/12, 06-MAR-2001.

RL DNAVAC RESEARCH INC, YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.

XX OS Artificial Sequence

CC PN JP 03075813-T/12

CC PD 06-MAR-2001

CC PR 06-SEP-2000 JP 2000006051

CC PT 06-SEP-1999 JP -99P 232231

CC PC YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA

CC C12N15/86,C12N15/45//A61K31/7105,A61K48/00

CC CC

CC FH Key

CC FT source 1..21

CC FT /organism="Artificial Sequence"

XX FH

XX FT source 1..21

XX FT /db_xref="taxon:32630"

XX /organism="synthetic construct"

SQ Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;

Query Match Best local Similarity 100.0%; Score 10; DB 23; Length 21;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

1:::|||||;

Db 9 CTTTCACCC 18

RESULT 15

AR099567

LOCUS AR099567

DEFINITION Sequence 94 from patent US 6077833. DNA linear PAT 14-FEB-2001

ACCESSION AR099567

VERSION AR099567.1 GI:12809333

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)

AUTHORS Bennett,C, Frank and Vickers,T,A.

TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein

JOURNAL Patent: US 6077833-A 94 20-JUN-2000;

FEATURES Location/Qualifiers

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GenCore version 5.1.4-p5-4578
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Om nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:06:05 ; Search time 168 Seconds

(without alignments)
134.048 Million cell updates/sec

Perfect score: US-09-702-498a-33-MOD
Sequence: 1. CuuuCACCCu 10
Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS2/gcadata/geneseq/geneseqn-emb1/NA1982.DAT;*
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23: /SIDS2/gcadata/geneseq/geneseqn-emb1/NA2001B.DAT;*
/SIDS2/gcadata/geneseq/geneseqn-emb1/NA2002.DAT;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10 22	AAT165896 Nucleotide sequence, SBO
2	10	100.0	10 22	AAT165896 S Sequence Oligo
3	10	100.0	22	AAT165896 S modified transcript
4	10	100.0	22	AAT165896 Sendai virus S seq
5	10	100.0	22	AAT177598 Sendai virus S modified transcript
6	10	100.0	24	AAT142655 Sendai virus S seq
7	10	100.0	24	AAT138107 Angiogenesis gene
8	10	100.0	10 24	ABP48812 DNA sequence #1 re
9	10	100.0	10 24	ABP33904 Sendai virus S Oli

RESULT	1	AA165896	ID	AA165896 standard; DNA; 10 BP.
		XX	XX	
		AA165896;	XX	
		DT	03-JAN-2002	(first entry)
		XX	XX	Nucleotide sequence of a synthetic oligonucleotide.
		XX	XX	Vaccine; Sendai virus vector; viral protein; immunodeficiency virus; AIDS; antigen gene; nasal mucosa; lymph node; ss.
		XX	OS	Synthetic.
		XX	PN	W0200172340-A1.
		XX	PD	04-OCT-2001.
		XX	PF	30-MAR-2001; 2001WO-JP02769.
		XX	PR	30-MAR-2000; 2000US-193127P.
		PA	(DNAV-) DNAV-EC RBS INC.	
		PA	(NINA-) JAPAN NAT INST INFECTIOUS DISEASES.	
		XX	Kano M, Matano T, Kato A, Nagai Y, Hasegawa M;	
		DR	WPI; 2001-616443/71.	
		XX	Viral protein of immunodeficiency virus-encoding Sendai virus vector-based AIDS virus vaccine for provision of efficient protective	

PT immunity comprises nasal administration to e.g. macaque to suppress
 PT onset and progress of AIDS
 XX Disclosure; Page 27; 92pp; Japanese.

PS

XX The specification describes a vaccine containing a sendai virus vector
 CC which encodes the viral protein of immunodeficiency virus. The vaccine
 CC is for treating AIDS, with expression of antigen gene mediated by the
 CC vector in nasal mucosa and local lymph nodes detected and
 CC antigen-specific cell-mediated response induced at significant
 CC level after vaccination. The present sequence represents an
 CC oligonucleotide which is used in the course of the invention.

XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10
 Db 1 CTTTACCCCT 10

RESULT 2

AAH73613
 ID AAH73613 standard; DNA; 10 BP.
 XX
 AC AAH73613;
 XX
 DT 27-SEP-2001 (first entry)
 DE DNA sequence, SEQ ID NO: 1.
 XX
 KW Gene therapy; vascular disorder; recombinant paramyxovirus vector; ds.
 XX
 OS Unidentified.
 XX
 PN WO200153491-A1.
 XX
 PD 26-JUL-2001.
 XX
 PR 11-JAN-2001; 2001WO-JP00087.
 XX
 PR 19-JAN-2000; 2000JP-0014136.
 XX
 PA (DNAV-) DNAVEC RBS INC.
 XX
 PI Masaki I, Yonemitsu Y, Sueishi K, Hasegawa M, Kinoh H;
 XX
 DR WPI; 2001-128799/34.
 XX
 PR Disclosure; Page 7; 42pp; English.
 XX
 CC The present invention relates to a composition for introducing exogenous
 CC genes to airway epithelia. The composition comprises a recombinant Sendai
 CC virus vector carrying an exogenous gene. The composition is useful in
 CC gene therapy. In particular, the composition is useful for treating
 CC cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep, bovine or
 CC monkey. The present sequence was used in the composition of the present
 CC invention as a transcription start sequence.
 XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10
 Db 1 CTTTACCCCT 10

RESULT 3

AAH23653
 ID AAH23653 standard; DNA; 10 BP.
 XX
 AC AAH23653;
 XX
 DR 07-AUG-2001 (first entry)
 DE S. sequence oligonucleotide used in a recombinant Sendai virus vector.
 XX
 KW Gene therapy; S sequence; airway epithelium; cystic fibrosis; ds.
 XX
 OS Parainfluenza virus.
 XX
 PN WO200132898-A2.

PR Disclosure; Page 7; 42pp; English.

XX
 CC The present invention relates to a composition for introducing exogenous
 CC genes to airway epithelia. The composition comprises a recombinant Sendai
 CC virus vector carrying an exogenous gene. The composition is useful in
 CC gene therapy. In particular, the composition is useful for treating
 CC cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep, bovine or
 CC monkey. The present sequence was used in the composition of the present
 CC invention as a transcription start sequence.
 XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10
 Db 1 CTTTACCCCT 10

RESULT 4

AAF86115
 ID AAF86115 standard; DNA; 10 BP.
 XX
 AC AAF86115;
 XX
 DR 21-JUN-2001 (first entry)
 DE Sendai virus S sequence oligonucleotide.

SO Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

DE

XX	Extracellular superoxide dismutase; EC-SOD; immunosuppressive; antiinflammatory; antiarthritic; antirheumatic; arthritis; colitis; systemic autoimmune disease; systemic lupus erythematosus; rheumatic myocarditis; progressive systemic sclerosis; dermatomyositis; Sjogren's syndrome; polyarteritis; Sendai virus; ss.	KW
OS	Parainfluenza virus.	
XX	CA2316518-A1.	
PN		
XX	01-MAR-2001.	
PD		
XX	01-MAR-2001.	
XX	31-AUG-2000; 2000CA-2316518.	
PR		
XX	01-SEP-1999; 99JP-0248032.	
PR		
XX	27-APR-2000; 2000CA-2304453.	
PA		
XX	(DNAV-) DNA VEC RES INC.	
PS		
XX	Yamauchi N, Fukumura M, Iyama S, Hasegawa M, Niitsu Y;	
XX	WPI; 2001-300717/32.	
PT		
XX	New EC-SOD proteins and nucleic acids encoding the protein useful in gene therapy for treating or preventing systemic autoimmune diseases, e.g. rheumatoid arthritis, colitis and systemic lupus erythematosus.	
PT		
XX	Disclosure; Page 24; 71pp; English.	
CC		
CC	This invention relates to a superoxide dismutase (SOD) protein which exists extracellularly and is termed EC-SOD, and the polynucleotide encoding it. SOD is the enzyme that catalyses the reaction involved in superoxide anion radical production. The invention includes a vector containing the EC-SOD coding sequence, and a method for treating or preventing systemic autoimmune diseases comprising administering the vector. Methods using the EC-SOD protein and DNA sequences result in immunosuppressive, anti-inflammatory, antiarthritic, and antirheumatic activity. The EC-SOD protein and nucleic acid encoding the protein are useful for treating systemic autoimmune diseases such as arthritis, rheumatoid arthritis, colitis, systemic lupus erythematosus, rheumatic myocarditis, progressive systemic sclerosis, dermatomyositis, mixed connective tissue disease, Sjogren's syndrome, polymyositis/polymyositis, which can be used in the construction of a vector containing the EC-SOD gene.	
CC		
CC	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	
CC	Query Match 100.0%; Score 10; DB 22; Length 10; Best Local Similarity 60.0%; Pred. No. 4.2e+03; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	
CC	QY 1 CUUCUACCCU 10	
CC	OY : : 10	
CC	Db 1 CTTTCAACCT 10	
SQ		
RESULT 5		
AAF77598		
ID	AAF77598 standard; DNA; 10 BP.	
XX		
XX	AAF77598;	
XX		
XX	29-MAY-2001 (first entry)	
XX		
DE	Modified transcription initiation site Paramyxovirus related oligo #18.	
XX	Transcription initiation sequence; viral vector; vaccine; therapy; ds.	
XX	Unidentified.	
XX		
PN	WO200118223-A1.	
XX	15-MAR-2001.	
PD		
XX	06-SEP-2000; 2000WO-JP06051.	
PF		
XX	06-SEP-1999; 99JP-0252231.	
PR		
XX	(DNAV-) DNAVEC RES INC.	
PA		
XX	Nagai Y, Kato A, Hasegawa M;	
PT		
XX	DR. WPI; 2001-244576/25.	
XX		
PT	Paramyxovirus vectors with modified transcription initiation sequences for increased expression of foreign genes in production of drugs and vaccines.	
PT		
XX	Disclosure; Page 17; 65pp; Japanese.	
PS		
XX	The present invention describes a paramyxovirus vector DNA in which the transcription initiation sequence has been modified to modify the expression of a gene located downstream of the transcription initiation sequence. This is useful in the production of mutant paramyxovirus vectors with elevated gene expression and a more rapid proliferation than the wild-type vector, which can then be used for more efficient production of drug substances and vaccines.	
XX		
SQ	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	
RESULT 6		
AAL47265		
ID	AAL47265 standard; DNA; 10 BP.	
XX		
XX	AC AAL47265;	
XX		
XX	30-AUG-2002 (first entry)	
XX		
DE	Sendai virus 5 sequence complement.	
XX		
XX	Sendai virus vector; gene therapy; antiinflammatory; inflammation; cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis; sclerosing peritonitis; prostatomegaly; multiple sclerosis; neuroprotective; immunosuppressive; antidiabetic; antirheumatic; transplant; refection; diabetes; chronic articular rheumatism; psoriasis; inflammatory enteropathy; systemic lupus erythematosus; litis; granulomatous disease; chronic nephritis; scleromyoma; hysterosomyoma; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.	
OS		
XX	Sendai virus.	
PN	WO200238122-A2.	
XX		
PD	16-MAY-2002.	
XX		
XX	08-NOV-2001; 2001WO-JP09786.	
XX		
PR	08-NOV-2000; 2000JP-033942.	
XX		
PR	(DNAV-) DNAVEC RES INC.	
PA		
XX	Griesenbach U, Ferrari S, Geddes DM, Alton EW, Hasegawa M, Hou X;	
PI		
XX	WPI; 2002-490069/52.	

XX	XX	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	XX	XX
PT	Query Match	100.0%; Score 10; DB 24; Length 10;	PT	Query Match
PT	Best Local Similarity	60.0%; Pred. No. 4.2e+03; Matches	PT	Best Local Similarity
PT	Matches	6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	PT	Matches
XX	PS	Disclosure: Page 17; 67pp; English.	XX	PS
CC	CC	The present invention relates to a paramyxovirus vector for gene transfer to cardiovascular system, in which expression product of gene comprised in vector is transferred to a site different from the site of administration through the bloodstream.	CC	CC
CC	CC	The vector is useful for transferring sequences such as IL-10 to the cardiovascular system, for treating inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis, prosatomegaly, multiple sclerosis, post transplant refection, diabetes, chronic articular rheumatism, psoriasis, inflammatory enteropathy, systemic lupus erythematosus, iritis, granulomatous disease, chronic nephritis, scleroderma, Mysteromyia, keloid and cirrosis. The present sequence is a DNA fragment used to produce the vector of the invention.	CC	CC
XX	SQ	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	XX	XX
Query Match	100.0%; Score 10; DB 24; Length 10;	Query Match	100.0%; Score 10; DB 24; Length 10;	
Best Local Similarity	60.0%; Pred. No. 4.2e+03; Matches	Best Local Similarity	60.0%; Pred. No. 4.2e+03; Matches	
Matches	6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	Matches	6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	
XX	OY	1 CUUUCACCCU 10	XX	OY
Db	1 CTTTCACCC 10	Db	1 CTTTCACCC 10	
RESULT 7	RESULT 8	RESULT 8	RESULT 9	RESULT 9
RAL38107	ABK48812	ABK48812	ABK48812	ABK48812
ID	ID	ID	ID	ID
RAL38107 standard; DNA; 10 BP.	ABK48812 standard; DNA; 10 BP.	ABK48812 standard; DNA; 10 BP.	ABK48812 standard; DNA; 10 BP.	ABK48812 standard; DNA; 10 BP.
XX	XX	XX	XX	XX
XX	AC	AC	AC	AC
AC	AAL38107;	AAL38107;	AAL38107;	AAL38107;
XX	DT	DT	DT	DT
DT	15-AUG-2002 (first entry)	15-JUL-2002 (first entry)	15-JUL-2002 (first entry)	15-JUL-2002 (first entry)
XX	DE	DE	DE	DE
DE	Angiogenesis gene containing paramyxovirus vector related oligo #1.	Method for gene transfer; skeletal muscle; paramyxovirus vector; gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective; myotropic; insulin-like growth factor; IGF; ds.	Method for gene transfer; skeletal muscle; paramyxovirus vector; gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective; myotropic; insulin-like growth factor; IGF; ds.	Method for gene transfer; skeletal muscle; paramyxovirus vector; gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective; myotropic; insulin-like growth factor; IGF; ds.
XX	AC	AC	AC	AC
AC	W0200231138-A1.	W0200231138-A1.	W0200231138-A1.	W0200231138-A1.
XX	OS	OS	OS	OS
OS	Unidentified.	Unidentified.	Unidentified.	Unidentified.
XX	PN	PN	PN	PN
PN	W0200242481-A1.	W0200242481-A1.	W0200242481-A1.	W0200242481-A1.
XX	PD	PD	PD	PD
PD	18-APR-2002.	18-APR-2002.	18-APR-2002.	18-APR-2002.
XX	PR	PR	PR	PR
PR	26-SEP-2001; 2001WO-JP08372.	26-SEP-2001; 2001WO-JP08372.	26-SEP-2001; 2001WO-JP08372.	26-SEP-2001; 2001WO-JP08372.
XX	PR	PR	PR	PR
PR	06-OCT-2000; 2000JP-0308533.	06-OCT-2000; 2000JP-0308533.	06-OCT-2000; 2000JP-0308533.	06-OCT-2000; 2000JP-0308533.
XX	PA	PA	PA	PA
PA	(DNAV-) DNAVAC RES INC.			
XX	PI	PI	PI	PI
PI	Hukumura M, Shiotani A, Maeda M, Hasegawa M;	Hukumura M, Shiotani A, Maeda M, Hasegawa M;	Hukumura M, Shiotani A, Maeda M, Hasegawa M;	Hukumura M, Shiotani A, Maeda M, Hasegawa M;
XX	DR	DR	DR	DR
DR	WPI; 2002-340180/37.	WPI; 2002-340180/37.	WPI; 2002-340180/37.	WPI; 2002-340180/37.
XX	PT	PT	PT	PT
PT	Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders -	Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders -	Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders -	Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders -
XX	PS	PS	PS	PS
PS	Disclosure: Page 14; 56pp; Japanese.			
XX	CC	CC	CC	CC
CC	The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after infection and is safe, non-infective and does not cause tumourigenesis. The present DNA sequence of unknown function is given in the specification of the present invention.	The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after infection and is safe, non-infective and does not cause tumourigenesis. The present DNA sequence of unknown function is given in the specification of the present invention.	The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after infection and is safe, non-infective and does not cause tumourigenesis. The present DNA sequence of unknown function is given in the specification of the present invention.	The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after infection and is safe, non-infective and does not cause tumourigenesis. The present DNA sequence of unknown function is given in the specification of the present invention.
XX	PS	PS	PS	PS
PS	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
XX	Query Match	100.0%; Score 10; DB 24; Length 10;	Query Match	100.0%; Score 10; DB 24; Length 10;
PT	Best Local Similarity	60.0%; Pred. No. 4.2e+03; Matches	Best Local Similarity	60.0%; Pred. No. 4.2e+03; Matches
PT	Matches	6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	PT	Matches
XX	OY	1 CUUUCACCCU 10	XX	OY
Db	1 CTTTCACCC 10	Db	1 CTTTCACCC 10	
RESULT 9	RESULT 9	RESULT 9	RESULT 9	RESULT 9
ABL3904	ABL3904	ABL3904	ABL3904	ABL3904
ID	ID	ID	ID	ID
XX	XX	XX	XX	XX
XX	CC	CC	CC	CC
CC	The invention relates to a paramyxovirus vector containing an angiogenesis gene, which can be used for gene therapy of ischaemia in tissues including brain, heart, lung, skeletal muscle and kidney. The expression of the virus vector is free from edema and specific tissues can be targeted. This polynucleotide sequence represents an artificial oligonucleotide relating to the paramyxovirus vector containing an angiogenesis gene FGF2 of the invention.	The invention relates to a paramyxovirus vector containing an angiogenesis gene, which can be used for gene therapy of ischaemia in tissues including brain, heart, lung, skeletal muscle and kidney. The expression of the virus vector is free from edema and specific tissues can be targeted. This polynucleotide sequence represents an artificial oligonucleotide relating to the paramyxovirus vector containing an angiogenesis gene FGF2 of the invention.	The invention relates to a paramyxovirus vector containing an angiogenesis gene, which can be used for gene therapy of ischaemia in tissues including brain, heart, lung, skeletal muscle and kidney. The expression of the virus vector is free from edema and specific tissues can be targeted. This polynucleotide sequence represents an artificial oligonucleotide relating to the paramyxovirus vector containing an angiogenesis gene FGF2 of the invention.	The invention relates to a paramyxovirus vector containing an angiogenesis gene, which can be used for gene therapy of ischaemia in tissues including brain, heart, lung, skeletal muscle and kidney. The expression of the virus vector is free from edema and specific tissues can be targeted. This polynucleotide sequence represents an artificial oligonucleotide relating to the paramyxovirus vector containing an angiogenesis gene FGF2 of the invention.

AC ABL39904;
 XX KW Tourette's Syndrome; attention deficit disorder; hyperactivity;
 DT KW post-traumatic stress disorder; PCR amplification; RFLP;
 XX KW restriction fragment length polymorphism; ss.
 DE Sendai virus S oligonucleotide SEQ ID NO:1.
 XX OS Synthetic.
 KW
 KW Sendai virus; virus vector; renal cell; paramyxovirus; gene transfer;
 KW gene therapy; kidney; nephrotoxic; antidiabetic; diabetes; nephopathy;
 KW chronic glomerulonephritis; glomerulosclerosis; Alport's syndrome;
 KW tubulointerstitial nephritis; ss.
 XX OS Parainfluenza virus.
 PN XX
 WO200200264-A1.
 XX
 XX
 PD 03-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-JP05513.
 XX
 PR 27-JUN-2000; 2000JP-0197870.
 PA XX
 PI (DNAV-) DNAVEC RES INC.
 XX
 Imai E, Isaka Y, Fukumura M, Hasegawa M;
 DR XX
 WPI; 2002-130841/17.
 XX
 PS PT
 PT Transferring a gene into renal cells, useful for gene therapy of a
 PT kidney to treat e.g. chronic glomerulonephritis, comprises using a
 virus vector particularly of paramyxovirus
 XX PS
 Example 1; Page 38; 75pp; Japanese.
 XX
 The present invention describes transferring a gene into renal cells
 comprising contacting a paramyxovirus vector with the renal cells,
 particularly by administration into blood vessels, especially the renal
 artery or into the urethra. Also described are: (1) a paramyxovirus
 vector for use in transferring a gene into renal cells; and
 (2) compositions for transferring a gene into renal cells comprising
 cells having the paramyxovirus vector or the vector. The method is used
 for transferring a gene into renal cells. The virus is applicable in
 gene therapy for the kidney to treat target diseases of e.g. chronic
 glomerulonephritis, diabetes, nephopathy, glomerulosclerosis,
 tubulointerstitial nephritis and Alport's syndrome. The transfer of a
 gene into renal cells is with high efficiency, and after brief exposure,
 the transferred gene is continuously expressed in renal cells over a
 long period of time. The present sequence represents a Sendai virus
 (parainfluenza virus) oligonucleotide which is used in an example from
 the present invention.
 XX
 Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
 XX
 Query Match 100.0%; Score 10; DB 24; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.2e+03; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUCUCACCCU 10
 Db 11 CTCACCC 2
 XX
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;
 XX
 Query Match 100.0%; Score 10; DB 15; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.3e+03; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUCUCACCCU 10
 Db 11 CTCACCC 2
 XX
 RESULT 11
 AAT18122_C
 ID AAT18122 standard; DNA; 11 BP.
 XX
 AC AAT18122;
 XX
 DT 22-AUG-1996 (first entry)
 XX
 DE Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).
 XX
 KW Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;
 KW PCR amplification of specific alleles; PASA; compulsive disorder;
 KW cocaine dependence; alcoholism; genetic susceptibility; ss.
 XX OS Homo sapiens.
 XX
 FH Key allele 6
 FT Location/qualifiers
 FT /*tag= a
 FT /note= "nucleotides 3203-3213 of DRD2 in which
 DE there is a T at the polymorphic position
 XX 3208".
 KW Human dopamine D2 receptor; genetic susceptibility; diagnosis;
 KW DRD2; compulsive disorder; alcoholism; cocaine dependence;
 XX
 PN US5500343-A.
 XX

PD 19-MAR-1996.
 XX
 PF 07-FEB-1990; 90US-0477057.
 XX
 PT Hepburn AG, Wang C;
 XX
 PR 24-JUN-1992; 92US-090983.
 PR 07-FEB-1990; 90US-0477057.
 XX
 DR 23-JAN-1992; 92US-0826222.
 XX
 PT (REGC) UNIV CALIFORNIA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Blum K, Noble EP, Sheridan PJ;
 XX
 DR WPI; 1996-171043/17.
 XX
 PT Detecting genetic potential susceptibility to cocaine dependence or alcoholism - by detecting human dopamine D2 receptor gene A1 or B1 allele in the subject's DNA
 XX
 PS Example 3; Column 45; 56pp; English.
 XX
 The dopamine D2 receptor DRD2(1n6-5x7) haplotype is comprised of two polymorphisms that are separated by 212 bp and span the junction of the intron 6 and exon 7 sequences. The first is a T or C allele at position 3208 and the second polymorphism is a T or C at position 3420, providing 4 possible haplotypes. Haplotype I is characterised by T at position 3208 and C at position 3420. The primers #3208 and #3420 specifically amplify a 241 bp fragment dopamine D2 receptor haplotype I which is associated with alcoholism. The primers are used in a claimed method for detecting genetic potential susceptibility to alcoholism in human subjects. In particular, amplification is carried out using the PASA technique (i.e. PCR amplification of specific Alleles). In related methods, genetic potential susceptibility to cocaine dependence can be detected by amplifying human dopamine D2 receptor A1 and B1 alleles (primers not specified).
 XX
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;
 XX
 Query Match 100 0%; Score 10; DB 17; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4. 3e-03;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CUUUCACCCU 10
 DB 11 CTTTCACCT 2
 XX
 RESULT 12
 AAX14846/C
 AAX14846 standard; DNA; 12 BP.
 XX
 AC AAX14846;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Triple helix forming nucleotides 394-395 of 23S rRNA gene.
 XX
 KW Triple-helix forming region; Triplex formation; DNA detection;
 KW identification; bacteria; oncogene; virus; ds;
 KW Leptospira interrogans.
 OS
 PN US5861244-A.
 XX
 PD 19-JAN-1999.
 XX
 PF 22-DEC-1993; 93US-0173489.
 XX
 PR 22-DEC-1993; 93US-0173489.
 PR 29-OCT-1992; 92US-0968436.
 XX
 PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
 XX
 PT Hepburn AG, Wang C;
 XX
 PR WPI; 1999-130384/11.
 XX
 PT Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria
 PT
 XX
 PS Disclosure; Columns 21-22; 168pp; English.
 XX
 CC The present sequence represents a potential triple-helix forming region.
 CC It can be used to demonstrate the assay of the invention. The assay
 CC comprises adding a sample containing double-stranded DNA test sequences,
 CC e.g. containing the present sequence, to an aqueous medium containing at
 CC least one complex of anchor DNA, attached to a solid support, and
 CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
 CC designed to form a triple strand structure with part of the test
 CC sequence. Triplex formation results in displacement of the reporter DNA
 CC which is detected as an indication of the presence of the DNA test
 CC sequence. The method is used to detect DNA sequences, particularly for
 CC identification of bacteria (by detecting genes for ribosomal RNA) in
 CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
 XX
 SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 other;
 XX
 Query Match 100 0%; Score 10; DB 20; Length 12;
 Best Local Similarity 60.0%; Pred. No. 4. 3e-03;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CUUUCACCCU 10
 DB 12 CTTTCACCT 3
 XX
 RESULT 13
 ABF05726/C
 ID ABF05726 standard; DNA; 13 BP.
 XX
 AC ABF05726;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PR 06-APR-2001; 2001WO-1B00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PT Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-65717/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pre-treated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention. CC NOTE: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences. XX

SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other; XX

Query Match 100 0%; Score 10; DB 23; Length 13; Best Local Similarity 60.0%; Pred. No. 4. 3e+03; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; QY 1 CUUUCACCCU 10 Db 13 CTTTCACCC 4

SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 other; XX

Query Match 100 0%; Score 10; DB 23; Length 13; Best Local Similarity 60.0%; Pred. No. 4. 3e+03; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; QY 1 CUUUCACCCU 10 Db 13 CTTTCACCC 4

Search completed: March 19, 2003, 00:07:18

Job time : 168 secs

Length 11;
; Indels 0; Gaps 0;
E HUMAN
NE IN
Sequence 262, Appl
Sequence 72, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 28, Appl
Sequence 142, Appl
Sequence 17, Appl
Sequence 2, Appl
Patient No. 5242798
Sequence 9, Appl
Sequence 57, Appl
Sequence 128, Appl
Sequence 1, Appl
Sequence 1, Appl

LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-09-326-186B-95

Query Match 100.0%; Score 10; DB 4; Length 19;
 Best Local Similarity 60.0%; Pred. No. 6. 1e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10
 Db 7 CTPTCACCC 16

RESULT 5
 US-08-777-266A-94
 ; Sequence 94, Application US/0877726A
 ; Patent No. 6077683
 ; GENERAL INFORMATION:
 ; APPLICANT: Clarence Frank Bennett
 ; APPLICANT: Timothy A. Vickers
 ; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Jane Massey Licata
 ; STREET: 210 Lake Drive East, Suite 201
 ; CITY: Cherry Hill
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777-266A
 ; FILING DATE: December 31, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: ISPH-0201
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (609) 779-2400
 ; TELEFAX: (609) 779-8488
 ; INFORMATION FOR SEQ ID NO: 94:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; ANTI-SENSE: Yes
 ; US-08-777-266A-94

Query Match 100.0%; Score 10; DB 4; Length 19;
 Best Local Similarity 60.0%; Pred. No. 6. 1e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10
 Db 7 CTPTCACCC 16

RESULT 5
 US-08-777-266A-94
 ; Sequence 94, Application US/0877726A
 ; Patent No. 6077683
 ; GENERAL INFORMATION:
 ; APPLICANT: Clarence Frank Bennett
 ; APPLICANT: Timothy A. Vickers
 ; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Jane Massey Licata
 ; STREET: 210 Lake Drive East, Suite 201
 ; CITY: Cherry Hill
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777-266A
 ; FILING DATE: December 31, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: ISPH-0201
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (609) 779-2400
 ; TELEFAX: (609) 779-8488
 ; INFORMATION FOR SEQ ID NO: 94:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; ANTI-SENSE: Yes
 ; US-08-777-266A-94

Query Match 100.0%; Score 10; DB 4; Length 22;
 Best Local Similarity 60.0%; Pred. No. 6. 2e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10
 Db 7 CTPTCACCC 16

RESULT 7
 US-07-952-442-7
 ; Sequence 7, Application US/07952442
 ; Patent No. 5374525
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalouli, Jean-Marc
 ; APPLICANT: Jeunemaitre, Xavier
 ; APPLICANT: Lifton, Richard P.
 ; APPLICANT: Soubrie, Florent
 ; APPLICANT: Kotelevtsev, Youri
 ; APPLICANT: Corval, Pierre
 ; TITLE OF INVENTION: Angiotensinogen Gene Variants and Predisposition to Essential Hypertension
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/952,442
 ; FILING DATE: 19920930
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Irene, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 19780-104502
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 23 base Pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

RESULT 6
 US-09-326-186B-94
 ; Sequence 94, Application US/09326186B

Db 13 CTTCAACCT 22

RESULT 8

US-08-269-766-7

; Sequence 7, Application US/08269766

; Patent No. 559584

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaire, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Sourrier, Florent

APPLICANT: Kotlevtsev, Youri

APPLICANT: Corvol, Pierre

TITLE OF INVENTION: Angiotensinogen Gene Variants and Predisposition to Essential Hypertension

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1/5.2 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/119,545A

FILING DATE: 7-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/269,766

FILING DATE: 01-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 19780-104502-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-319-545A-7

Query Match 100.0%; Score 10; DB 1; Length 23;

Best Local Similarity 60.0%; Pred. No. 6.2e+02;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

Db 13 CTTCAACCT 22

RESULT 9

US-08-319-545A-7

; Sequence 7, Application US/08319545A

; Patent No. 5595168

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaire, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Sourrier, Florent

APPLICANT: Kotlevtsev, Youri

APPLICANT: Corvol, Pierre

TITLE OF INVENTION: Method to Determine Predisposition to Hypertension

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1/5.2 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/119,545A

FILING DATE: 7-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/269,766

FILING DATE: 01-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 19780-104502-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-319-545A-7

Query Match 100.0%; Score 10; DB 1; Length 23;

Best Local Similarity 60.0%; Pred. No. 6.2e+02;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

Db 13 CTTCAACCT 22

RESULT 10

US-09-092-988-7

; Sequence 7, Application US/09092988

; Patent No. 5598145

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaire, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Sourrier, Florent

APPLICANT: Kotelertsev, Youri
 APPLICANT: Corvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 TITLE OF INVENTION: to Hypertension
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1/5.2 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/092,988
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/
 FILING DATE: 08-TUN-1998
 PRIORITY APPLICATION NUMBER: 08/319,545
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 19780-104502-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-092-988-7

Query Match 100.0%; Score 10; DB 2; Length 23;
 Best Local Similarity 60.0%; Pred. No. 6.2e+02;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUUUCACCCU 10
 1:::|||||:
 Db 13 CTTTCACCC 22

RESULT 11
 US-09-106-216-7
 ; Sequence 7, Application US/09106216
 ; Patent No. 615386
 ; GENERAL INFORMATION:
 APPLICANT: Halouel, Jean-Marc
 APPLICANT: Jeunemaitre, Xavier
 APPLICANT: Lofton, Richard P.
 APPLICANT: Soubrrier, Florent
 APPLICANT: Kotelertsev, Youri
 APPLICANT: Corvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 TITLE OF INVENTION: to Hypertension
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1/5.2 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/429,034
 FILING DATE:
 CLASSIFICATION:

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/106,216
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/
 FILING DATE: 08-TUN-1998
 PRIORITY APPLICATION NUMBER: 08/319,545
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 19780-104502-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-6040
 TELEFAX: 202-783-6031
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "primer"
 US-09-106-216-7

Query Match 100.0%; Score 10; DB 3; Length 23;
 Best Local Similarity 60.0%; Pred. No. 6.2e+02;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUUUCACCCU 10
 1:::|||||:
 Db 13 CTTTCACCC 22

RESULT 12
 US-09-429-034-7
 ; Sequence 7, Application US/09429034
 ; Patent No. 616527
 ; GENERAL INFORMATION:
 APPLICANT: Halouel, Jean-Marc
 APPLICANT: Jeunemaitre, Xavier
 APPLICANT: Lofton, Richard P.
 APPLICANT: Soubrrier, Florent
 APPLICANT: Kotelertsev, Youri
 APPLICANT: Corvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 TITLE OF INVENTION: to Hypertension
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1/5.2 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/429,034
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,545
 FILING DATE: 7-OCT-1994
 APPLICATION NUMBER: US 07/952,442
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 19780-104502-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-662-8300

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TOPOLGY: linear
 STRANDEDNESS: single
 TYPE: nucleic acid
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-429-034-7

RESULT 13
 US-08-777-266A-93
 Sequence 93, Application US/08777266A
 Patent No. 607833

GENERAL INFORMATION:
 APPLICANT: Clarence Frank Bennett
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins
 NUMBER OF SEQUENCES: 125
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Jane Massey Licata
 STREET: 210 Lake Drive East, Suite 201
 CITY: Cherry Hill
 STATE: NJ
 COUNTRY: USA
 ZIP: 08002

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/777,266A
 FILING DATE: December 31, 1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 32,257
 REFERENCE/DOCKET NUMBER: ISPH-0201
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 779-4400
 TELEFAX: (609) 779-8488
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24

RESULT 14
 US-09-326-186B-93
 Sequence 93, Application US/09326186B
 Patent No. 6319906

GENERAL INFORMATION:
 APPLICANT: Bennett, Clarence Frank
 APPLICANT: Vickers, Timothy A.
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins
 FILE REFERENCE: ISPH-0376
 CURRENT APPLICATION NUMBER: US/09/326,186B
 CURRENT FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 08/777,266
 PRIOR FILING DATE: 1996-12-31
 NUMBER OF SEQ ID NOS: 226
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 93
 LENGTH: 24

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-326-186B-93

RESULT 15
 US-08-205-697A-39/C
 Sequence 39, Application US/08205697A
 Patent No. 6218510

GENERAL INFORMATION:
 APPLICANT: Sharpe, Arlene H.
 APPLICANT: Borriello, Francescopaolo
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LARIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,697A

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BWI-120

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

MOLECULE TYPE: cDNA

NAME/KEY:

LOCATION: 107..124

US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;

Best Local Similarity 60.0%; Pred. No. 6.9e+02;

Matches 6; Conservative 4; Mismatches 0; Indels 0;

Gaps 0; QY 1 CUCUCACCCU 10

Db 13 CTTTCACCT 4

Search completed: March 19, 2003, 01:26:21
Job time : 38 secs

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GenCore version 5.1.4_P5_4578
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OM nucleic - nucleic search, using sw model

Run on:

March 19, 2003, 00:40:46 ; Search time 51.5 Seconds

(without alignments)
 136.284 Million cell updates/sec

Title: US-09-702-498a-33-MOD
 Perfect score: 10

Sequence: 1 CUUUCACCCU 10

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 102604

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pupbna/PCT06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pupbna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pupbna/US05_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pupbna/US07_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pupbna/US06_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pupbna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pupbna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pupbna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pupbna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10	Sequence 63, Appl
2	10	100.0	10	Sequence 63, Appl
3	10	100.0	10	Sequence 63, Appl
4	10	100.0	21	Sequence 1, Appl
5	10	100.0	30	Sequence 21, Appl
6	10	100.0	47	Sequence 43, Appl
7	10	100.0	47	Sequence 44, Appl
8	10	100.0	47	Sequence 44, Appl
9	10	100.0	47	Sequence 44, Appl
10	10	100.0	63	Sequence 44, Appl
11	10	100.0	69	Sequence 44, Appl
12	10	100.0	69	Sequence 44, Appl
13	10	100.0	69	Sequence 44, Appl
14	10	100.0	69	Sequence 44, Appl
15	10	100.0	69	Sequence 44, Appl
16	10	100.0	72	Sequence 2, Appl
17	10	100.0	72	Sequence 34, Appl
18	10	100.0	72	Sequence 51, Appl
19	10	100.0	72	Sequence 52, Appl

ALIGMENTS

C	20	10	100.0	72	9	US-09-966-930-51	Sequence 51, Appl
C	21	10	100.0	72	9	US-09-966-930-52	Sequence 52, Appl
C	22	10	100.0	72	10	US-09-843-922-3	Sequence 3, Appl
C	23	10	100.0	74	9	US-09-966-277-31	Sequence 31, Appl
C	24	10	100.0	74	9	US-09-966-277-32	Sequence 32, Appl
C	25	10	100.0	74	9	US-09-966-930-31	Sequence 31, Appl
C	26	10	100.0	74	9	US-09-966-930-32	Sequence 32, Appl
C	27	10	100.0	80	9	US-09-966-277-18	Sequence 18, Appl
C	28	10	100.0	112	10	US-09-783-590-8499	Sequence 8499, AP
C	29	10	100.0	114	10	US-09-864-761-28324	Sequence 28324, A
C	30	10	100.0	116	10	US-09-164-761-24131	Sequence 24131, A
C	31	10	100.0	117	10	US-09-783-590-7779	Sequence 17517, A
C	32	10	100.0	124	9	US-09-962-669-39	Sequence 39, Appl
C	33	10	100.0	124	10	US-09-837-867A-39	Sequence 39, Appl
C	34	10	100.0	130	10	US-09-764-846-334	Sequence 334, AP
C	35	10	100.0	132	10	US-09-969-313-1040	Sequence 1040, AP
C	36	10	100.0	140	10	US-09-923-873-3943	Sequence 3943, AP
C	37	10	100.0	143	10	US-09-783-590-7779	Sequence 7779, AP
C	38	10	100.0	148	10	US-09-864-761-23518	Sequence 23518, A
C	39	10	100.0	165	9	US-09-665-935-156	Sequence 156, APP
C	40	10	100.0	165	9	US-09-878-178-156	Sequence 156, APP
C	41	10	100.0	165	10	US-09-864-761-30761	Sequence 30761, A
C	42	10	100.0	165	10	US-09-878-574-11498	Sequence 11498, A
C	43	10	100.0	174	10	US-09-783-590-6678	Sequence 6678, AP
C	44	10	100.0	180	10	US-09-983-965-2379	Sequence 2379, AP

Query Match 100.0% ; Score 10; DB 9; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1, 10^3 ; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Sequence 34, Appl

Db 1 :::::::::: 10

RESULT 2
US-09-966-930-63

; Sequence 63, Application US/09666930

; GENERAL INFORMATION:

; APPLICANT: KITAZATO, Kalo

; APPLICANT: SHU, Tsugumine

; APPLICANT: KUMA, Hidekazu

; APPLICANT: UEDA, Yasuji

; APPLICANT: ASAKAWA, Makoto

; APPLICANT: HASEGAWA, Mamoru

; APPLICANT: IIDA, Akihiro

; APPLICANT: HITOMA, Takahiro

; APPLICANT: INOUE, Makoto

TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

FILE REFERENCE: 500/6-029001

CURRENT APPLICATION NUMBER: US/09/966,930

PRIOR APPLICATION NUMBER: PCT/JP00/03194

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/283451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200740

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-63

Query Match 100.0%; Score 10; DB 9; Length 10;

Best Local Similarity 60.0%; Pred. No. 1.5e+03;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

Db 1 CTTTCACCC 10

RESULT 3

US-09-823-699-1

; Sequence 1, Application US/09823699

; Patent No. US2003002143A1

; GENERAL INFORMATION:

; APPLICANT: Kano, Munehide

; APPLICANT: Matano, Tetsuro

; APPLICANT: Kato, Atsushi

; APPLICANT: Nagai, Yoshiyuki

; APPLICANT: Hasegawa, Mamoru

TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus

FILE REFERENCE: 5026/02/2002

CURRENT APPLICATION NUMBER: US/09/823-699

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 60/193,127

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: artificially synthesized sequence

US-09-823-699-1

Db 1 CTTTCACCC 10

RESULT 4

US-09-972-331-21/c

; Sequence 21, Application US/09972331

; Patent No. US20020091083A1

; GENERAL INFORMATION:

; APPLICANT: HIGASHI, KIYOSHI

; APPLICANT: KONATSU, KENGO

TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING

FILE REFERENCE: 7372/72170

CURRENT APPLICATION NUMBER: US/09/972,331

CURRENT FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: JP 2000/310624

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: DESIGNED OLIGOONUCLEOTIDE PRIMER TO SYNTHESIZE

US-09-972-331-21

Query Match 100.0%; Score 10; DB 10; Length 21;

Best Local Similarity 60.0%; Pred. No. 1.7e-03;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

Db 11 CTTTCACCC 2

RESULT 5

US-09-988-115A-43

; Sequence 43, Application US/09988115A

; Publication No. US2003003734A1

; GENERAL INFORMATION:

; APPLICANT: Robl, James M.

; APPLICANT: Goldsby, Richard A.

; APPLICANT: Ferguson, Stacy E.

; APPLICANT: Kuroiwa, Yoshima

; APPLICANT: Tominaka, Kazuma

; APPLICANT: Isihara, Isao

TITLE OF INVENTION: Expression of Xenogenous (Human) Immunoglobulins in Cloned, Transgenic Ungulates

FILE REFERENCE: 50195/008003

CURRENT APPLICATION NUMBER: US/09/988-115A

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,625

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: US 60/256,458

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/714,185

PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: US 60/166,410

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 43

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetic Primer
; US-09-988-115A-43

Query Match 100.0%; Score 10; DB 9; Length 30;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10
Db 11 CTTTCACCC 20

RESULT 6
US-09-966-277-43/c
Sequence 43, Application US/09966277
Patent No. US20020169306A1
GENERAL INFORMATION:
APPLICANT: KITAZATO, Kai
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
APPLICANT: ASAKAWA, Makoto
APPLICANT: ITADA, Akihiko
APPLICANT: TOKITOU, Fumino
APPLICANT: HIRATA, Takahiro
APPLICANT: TOKUSUMI, Tsuyoshi
APPLICANT: INOUE, Makoto
TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
FILE REFERENCE: 50026/028001
CURRENT APPLICATION NUMBER: US/09/966, 277
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/JP00/03195
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: JP 11/200739
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 47
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-44
QY 1 CUUUCACCCU 10
Db 35 CTTTCACCC 44

RESULT 8
US-09-966-930-43/c
Sequence 43, Application US/09966930
Publication No. US20030022376A1
GENERAL INFORMATION:
APPLICANT: KITAZATO, Kai
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
APPLICANT: ASAKAWA, Makoto
APPLICANT: HASEGAWA, Mamoru
APPLICANT: ITADA, Akihiko
APPLICANT: HIRATA, Takahiro
APPLICANT: INOUE, Makoto
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
FILE REFERENCE: 50026/029001
CURRENT APPLICATION NUMBER: US/09/966, 930
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/JP00/03194
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: JP 2001/283451
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: JP 11/200740
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 47
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-43
Query Match 100.0%; Score 10; DB 9; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 CUUUCACCCU 10
Db 13 CTTTCACCC 4

RESULT 7
US-09-966-277-44
Sequence 44, Application US/09966277
Patent No. US20020169306A1
GENERAL INFORMATION:
APPLICANT: KITAZATO, Kai
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
APPLICANT: ASAKAWA, Makoto
APPLICANT: HASEGAWA, Mamoru
APPLICANT: ITADA, Akihiko
APPLICANT: TOKITOU, Fumino

Db 13 CTTTCACCT 4

Query Match 100.0%; Score 10; DB 10; Length 63;
Best Local Similarity 60.0%; Prc. No. 1.9e-03;
Matches 6; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;

RESULT 9
US-09-966-930-44
; sequence 44, Application US/09966930
; Publication No. US20030022376A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kaio
; APPLICANT: SHU, Tsugumine
; APPLICANT: UEDA, Yesuji
; APPLICANT: KUMA, Hidekazu
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: TIDE, Akihiro
; APPLICANT: HIRATA, Takahiro
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
; FILE REFERENCE: 50025/029001
; CURRENT APPLICATION NUMBER: US/09/966,930
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/JP00/03194
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: JP 2001/283451
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING NUMBER: JP 11/200740
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-930-44

Query Match 100.0%; Score 10; DB 9; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10
Db 35 CTTTCACCT 44

RESULT 10
US-09-823-699-10
; Sequence 10, Application US/09823699
; Patent No. US20020002143A1
; GENERAL INFORMATION:
; APPLICANT: Kano, Munehide
; APPLICANT: Matano, Tetsuro
; APPLICANT: Kato, Atsushi
; APPLICANT: Nada, Yoshiyuki
; APPLICANT: Hasegawa, Mamoru
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 50026/022002
; CURRENT APPLICATION NUMBER: US/09/823,699
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,127
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificially synthesized sequence
US-09-823-699-10

Query Match 100.0%; Score 10; DB 9; Length 63;
Best Local Similarity 60.0%; Prc. No. 1.9e-03;
Matches 6; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10
Db 17 CTTTCACCT 26

RESULT 11
US-09-471-840-2
; Sequence 2, Application US/09471840
; Patent No. US20020081/06A1
; GENERAL INFORMATION:
; APPLICANT: NAGAI, Yoshiyuki
; APPLICANT: KATO, Atsushi
; APPLICANT: MURAI, Fukashi
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: SAKATA, Tsuneki
; APPLICANT: HASEGAWA, Mamoru
; TITLE OF INVENTION: Negative Strand RNA Viral Vector Having
; FILE REFERENCE: 50026/004002
; CURRENT APPLICATION NUMBER: US/09/471,840
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: JP HEI 7-308315
; EARLIER FILING DATE: 1995-10-31
; EARLIER APPLICATION NUMBER: PCT/JP96/03068
; EARLIER FILING DATE: 1995-10-22
; EARLIER APPLICATION NUMBER: 03/070,938
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (35)...(35)
; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.
US-09-471-840-2

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10
Db 17 CTTTCACCT 26

RESULT 12
US-09-471-840-4
; Sequence 4, Application US/09471840
; Patent No. US20020081706A1
; GENERAL INFORMATION:
; APPLICANT: NAGAI, Yoshiyuki
; APPLICANT: KATO, Atsushi
; APPLICANT: MURAI, Fukashi
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: SAKATA, Tsuneki
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: SHIODA, Tatsuo
; TITLE OF INVENTION: Negative Strand RNA Viral Vector Having
; FILE REFERENCE: 50026/004002
; CURRENT APPLICATION NUMBER: US/09/471,840
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: JP HEI 7-308315
; EARLIER FILING DATE: 1995-10-31
; EARLIER APPLICATION NUMBER: PCT/JP96/03068

; EARLIER FILING DATE: 1995-10-22
; EARLIER APPLICATION NUMBER: 09/070,938
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Chemical synthesis
; US-09-471-840-4

Query Match 100.0%; Score 10; DB 10; Length 69;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 4; Mismatches 0;
 Qy 1 CUUUCACCCU 10
 Db 16 CTTTCACCT 25

RESULT 13
 US-09-728-207-2
 ; Sequence 2, Application US/09728207
 ; Patent No. US2002009576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGAI, Yoshiyuki
 ; APPLICANT: KATO, Atsushi
 ; APPLICANT: MURAI, Fukashi
 ; APPLICANT: SAKATA, Tsuneaki
 ; APPLICANT: HASEGAWA, Mamoru
 ; APPLICANT: SHIOKA, Tatsuo
 ; TITLE OF INVENTION: Recombinant Sendai Virus
 ; FILE REFERENCE: 50026/005001
 ; CURRENT APPLICATION NUMBER: US/09/728,207
 ; CURRENT FILING DATE: 2000-12-01
 ; PRIORITY NUMBER: US/09/071,591
 ; PRIORITY FILING DATE: 1998-05-01
 ; PRIORITY APPLICATION NUMBER: JP HEI 7-285417
 ; PRIORITY FILING DATE: 1995-11-01
 ; PRIORITY APPLICATION NUMBER: PCT/JP96/03069
 ; PRIORITY FILING DATE: 1996-10-22
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 69
 ; TYPE: DNA
 ; ORGANISM: Human immunodeficiency virus
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (35)::(35)
 ; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.
; US-09-728-207-2

Query Match 100.0%; Score 10; DB 10; Length 69;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 4; Mismatches 0;
 Qy 1 CUUUCACCCU 10
 Db 16 CTTTCACCT 25

RESULT 14
 US-09-728-207-2
 ; Sequence 2, Application US/09728207
 ; Patent No. US2002009576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGAI, Yoshiyuki
 ; APPLICANT: KATO, Atsushi
 ; APPLICANT: MURAI, Fukashi
 ; APPLICANT: SAKATA, Tsuneaki
 ; APPLICANT: HASEGAWA, Mamoru
 ; APPLICANT: SHIOKA, Tatsuo
 ; TITLE OF INVENTION: Negative Strand RNA Viral
 ; TITLE OF INVENTION: Vector Having Autonomous Replication Capability
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Clark & Elbing LLP
 ; STREET: 176 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/070,938
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-308315
 ; FILING DATE: 31-OCT-1995
 ; APPLICATION NUMBER: JP96/03068
 ; FILING DATE: 22-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 50026/004001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10
|:::|||||:
Db 17 CTTGACCC 26

Search completed: March 19, 2003, 02:47:57
Job time : 51.5 secs

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Om nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:53:50 : Search time 1320.5 Seconds
(without alignments)
122.647 Million cell updates/sec

Title: us-09-702-498a-33-mod

Perfect score: 10

Sequence: 1 CuuuCACCCU 10

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 16154066 seqs, 809743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estthm:*

3: em_estin:*

4: em_estmu:*

5: em_estcov:*

6: em_estpli:*

7: em_estro:*

8: em_htcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_liv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mean:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	28	17 TA285H02Q
2	10	100.0	38	17 A2332275
3	10	100.0	43	17 AL754476
4	10	100.0	67	17 A2805524
5	10	100.0	68	10 BE138421
6	10	100.0	72	13 BI783611

RESULTS

RESULT 1

TA285H02Q

LOCUS TA285H02Q

DEFINITION T. brucei sheared genomic DNA clone 285h02, reverse sequence, genomic survey sequence.

ACCESSION AL884543

VERSION AL884543.1

VERSION GI:11853036

KEYWORDS GSS.

SOURCE

ORGANISM Trypanosoma brucei.

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 28)

AH11, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Melville.S.E., Rajandream.M.A. and Barrell.B.G.

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TBR9274 cut at 10.1) was mechanically sheared to give a tight size distribution (~ 4 kb). The $v + i$ method used for the library construction is described in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of *T. brucei* sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source

1. .28

/organism="Trypanosoma brucei"

/strain="TREU027"

/db_xref="taxon:5691"

/clone="85h02"

/clone="85h02"

BASE COUNT

5

a

10

c

2

g

11

t

processed for submission. T-DNA derived sequences were removed, and selected for amplicin resistance.

BASE COUNT 8 a 10 c 8 g 17 t
ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 43;
Best Local Similarity 60.0%; Pred. No. 8.5e+04;
Matches 6; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10
Db 33 CTTTCACCC 42

RESULT 4
AZB05524/c
LOCUS AZB05524 2M06P22R Mouse 10kb plasmid UGGC1M library Mus musculus genomic
DEFINITION clone UGGC2M06P22R, DNA sequence.
ACCESSION AZB05524
VERSION AZB05524.1 GI:12966335
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 67)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm: 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: p column: 22
Seq primer: CACCCAGGAAACACTATGACC
Class: plasmid ends

FEATURES
Source
1. .07
/organism="Mus musculus"
/strain="C57BL/6"
/ab_xref="taxon:10090"
/clone="UGGC2M06P22"
/clone_lib="Mouse 10kb plasmid UGGC1M library"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nihares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (pG4721149b1A129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for amplicin resistance.

BASE COUNT 23 a 13 c 17 g 14 t
ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 60.0%; Pred. No. 9.4e+04;
Matches 6; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 CUPUCACCCU 10
Db 34 CTTTCACCC 25

RESULT 5
BEL38421/c
LOCUS BEL38421 2M06P22R Homo sapiens mRNA linear EST 21-JUN-2000
DEFINITION X74904.x2 NCI_CGAP_Ov26 Homo sapiens mRNA clone IMAGE:2765910 3', mRNA sequence.
ACCESSION BEL38421
VERSION BEL38421.1 GI:8600921
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 68)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/nciccgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@remall.nih.gov
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL, send email to: info@image.lnl.gov
Possible reversed clone: polyT not found
Seq primer: -400P from Gibco.
Location/Qualifiers

FEATURES
Source
1. .68
/organism="Homo sapiens"
/clone="IMAGE:2765910"
/ab_xref="taxon:9606"
/clone="NCI_CGAP_Ov26"
/sex="female"
/tissue_type="papillary serous carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAM1; mRNA made from papillary serous ovarian carcinoma; cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

BASE COUNT 26 a 8 c 22 g 12 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 68;
Best Local Similarity 60.0%; Pred. No. 9.4e+04;
Matches 6; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10

Db 57 CTTTCACCC 48

RESULT 6
B1783611
LOCUS B1783611

72 bp

mRNA

linear EST 26-SEP-2001

DEFINITION	Kh35e05.y1 Ascaris suum male head pAMP1 v2 Chiapelli McCarter	ACCESSION	AZ781553
ORGANISM	Ascaris suum	VERSION	AZ781553.1
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea	KEYWORDS	GSS.
LOCUS	Ascaridida; Ascaris.	VERSION	house mouse.
DEFINITION	1 (bases 1 to 72)	AUTHORS	Mus musculus
COMMENT	McCarte,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marr,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsakareliashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steppoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Wilson,R.	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	The Washington Univ. Nematode EST Project, 1999	REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
COMMENT	Unpublished (1999)	AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
JOURNAL	The Washington Univ. Nematode EST Project, 1999	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT	Contact: McCarter JP	JOURNAL	Plasmid inserts
JOURNAL	Washington Univ. Nematode EST Project, 1999	COMMENT	Unpublished (2000)
COMMENT	Washington University School of Medicine	CONTACT	Contact: Robert B. Weiss
JOURNAL	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	ORGANISM	University of Utah Genome Center
COMMENT	Tel: 314 286 1800	FEATURES	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
COMMENT	Fax: 314 286 1810	source	84112, USA
FEATURES	source	REFERENCE	Tel: 801 585 5606
source	The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@hspb.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD.	KEYWORDS	Fax: 801 585 7177
source	Seq Primer: -40RP from Gibco	ORGANISM	Email: daunne@genetics.utah.edu
source	High quality sequence stop: 58.	FEATURES	Insert Length: 10000 Std Error: 0.00
source	location/Qualifiers	source	Plate: 021; Row: I; Column: 03
source	1. .72	source	Class: plasmid ends
source	1. /organism="Ascaris suum"	source	Seq Primer: CGTTGAAACACGGCCAGT
source	/db_xref="taxon:6253"	source	High quality sequence stop: 72.
source	/clone_lib="Ascaris suum male head pAMP1 v2 Chiapelli	source	Location/Qualifiers
source	McCarte,"	source	1. .72
source	/sex="Male"	source	/organism="Mus musculus"
source	/tissue_type="Head"	source	/strain="C57BL/6J"
source	/dev_stage="Adult"	source	/db_xref="taxon:10090"
source	/lab_host="DH10B"	source	/clone="UUCG2MM021103"
note	"Vector: PAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@hspb.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD."	source	/clone.lib="Mouse 10 kb plasmid UGCGC library"
note	University in Baltimore, MD.	source	/sex="Male,"
note	10 a 22 c 15 g 25 t	source	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
note	BASE COUNT	source	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/Resource/documents/charges/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 1cm orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWNA2 (g11432114gb.fab129072.1), a copy-number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
note	ORIGIN	source	5 a 26 c 3 g 38 t
note	Query Match	source	Query Match
note	Best Local Similarity	source	Best Local Similarity
note	60.0%; Pred. No. 9 5e+04;	source	60.0%; Pred. No. 9 5e+04;
note	Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	source	Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
note	Qy 1 CTTUCACCCU 10	source	Qy 1 CTTUCACCCU 10
note	Db 26 CTTTCACCC 35	source	Db 34 CTTTCACCC 43
RESULT 7		RESULT 8	
AZ781553	AZ781553 72 bp DNA linear GSS 16-FEB-2001	B36161/c	B36161 73 bp DNA linear GSS 17-OCT-1997
LOCUS	2M02103F Mouse 10kb plasmid UGCGC library Mus musculus genomic clone UGCG2MM021103 F, DNA sequence.	DEFINITION	HS-038-A1-ELL-MF.ab1 CIR Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 820 Col=21 Row=1, DNA sequence.

Best Local similarity 60.0%; Pred. No. 1e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CUUUCACCU	10
	1	::::: :	
Db	31	CTTTCACCT	40

Search completed: March 19, 2003, 01:24:58
Job time : 1321.5 secs

GenCore version 5.1.4-p5_4578
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
Run on: March 18, 2003, 23:07:15 ; search time 991 seconds
(without alignments)
293.671 Million cell updates/sec

Title: US-09-702-498A-33

Perfect score: 10
Sequence: 1 CTTTCACCCCT 10

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: GenEmbl:*

2: gb_ba:*

3: gb_hhg:*

4: gb_ln:*

4: gb_on:*

5: gb_ov:*

6: gb_pt:*

7: gb_ph:*

8: gb_pj:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_wi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_sts:*

29: em_v1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pjh:*

35: em_htg_rcd:*

36: em_htg_men:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

RESULT 1
AX134713

LOCUS AX134713 DEFINITION Sequence 1 from Patent WO0132898. 10 bp
ACCESSION AX134713 VERSION AX134713.1 GI:14271230
KEYWORDS SOURCE synthetic construct.
ORGANISM synthetic construct.
ARTIFICIAL SEQUENCES

REFERENCE 1 (bases 1 to 10)
AUTHORS Yonemitsu, Y., Hasagawa, M. and Alton, E.
TITLE Recombinant sendai virus vector for introducing exogenous genes to
airway epithelia

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0132898-A 1 10-MAY-2001;

FEATURES	Dnavec	Research Inc. (JP)
SOURCE	Location/Qualifiers	
QY	1	CTTTCACCT 10
DEFINITION	/organism="synthetic construct"	
VERSION	11	CTTTCACCT 2
BASE COUNT	1	a 5 c 0 g 4 t
ORIGIN		
RESULT 2		
LOCUS	AX477327	10 bp
DEFINITION	Sequence 1 from Patent WO0238726.	DNA
ACCESSION	AX477327	linear
VERSION	AX477327.1	PAT 12-AUG-2002
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	Griesenbach,U., Ferrari,S., Geddes,D.M., Alton,E.W., Hasegawa,M. and Hou,X.	
TITLE	paramyxovirus vector for gene transfer to the cardiovascular system	
JOURNAL	Patent WO 0238726-A 116-MAY-2002;	
FEATURES		
SOURCE	1. .10 'organism="synthetic construct"' 'db_xref="txon:32630'"	
BASE COUNT	1	a 5 c 0 g 4 t
ORIGIN		
RESULT 3		
LOCUS	118631	11 bp
DEFINITION	Sequence 1 from Patent US 5500343.	DNA
ACCESSION	118631	linear
VERSION	118631.1	PAT 07-OCT-1996
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	Blum,K., Noble,E.P. and Sheridan,P.J.	
TITLE	Allelic association of the human dopamine(D2) receptor gene in compulsive disorders	
JOURNAL	Patent: US 5500343-A 1 19-MAR-1996;	
FEATURES		
SOURCE	Location/Qualifiers 1. .11 'organism="unknown"'	
BASE COUNT	4	a 0 c 6 g 1 t
ORIGIN		
RESULT 4		
LOCUS	AR030044	12 bp
DEFINITION	Sequence 233 from patent US 5861244.	DNA
ACCESSION	AR030044	linear
VERSION	AR030044.1	PAT 29-SEP-1999
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	Wang,C.-G. and Hepburn,A.G.	
TITLE	Genetic sequence assay using DNA triple strand formation	
JOURNAL	Patent: US 5861244-A 233 19-JAN-1999;	
FEATURES		
SOURCE	1. .12 'organism="unknown"'	
BASE COUNT	5	a 0 c 6 g 1 t
ORIGIN		
RESULT 5		
LOCUS	AR099568	19 bp
DEFINITION	Sequence 95 from patent US 6077833.	DNA
ACCESSION	AR099568	linear
VERSION	AR099568.1	PAT 14-FEB-2001
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	Bennett,C.Frank. and Vickers,T.A.	
TITLE	Oligonucleotide compositions and methods for the modulation of the expression of B7 protein	
JOURNAL	Patent: US 6077833-A 95 20-JUN-2000;	
FEATURES		
SOURCE	Location/Qualifiers 1. .19 'organism="unknown"'	
BASE COUNT	4	a 6 c 4 g 5 t
ORIGIN		
RESULT 6		
LOCUS	AR178849	19 bp
DEFINITION	Sequence 95 from patent US 6319906.	DNA
ACCESSION	AR178849	linear
VERSION	AR178849.1	PAT 20-APR-2002
Query Match	100.0%	Score 10; DB 6; Length 11;

KEYWORDS SOURCE unknown.
ORGANISM undefined.

REFERENCE 1 (bases 1 to 19)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7-protein
JOURNAL Patent: US 6319906-A 95 20-NOV-2001;
FEATURES Source 1..19
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BASE COUNT 4 a 6 c 4 g 5 t
ORIGIN 1 CTTTCACCT 10
/db_xref="Taxon:32630"
/note="primer"

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Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 7 CTTTCACCT 16

RESULT 7
AX108449
LOCUS AX108449
DEFINITION Sequence 12 from Patent WO0123548.
ACCESSION AX108449
VERSION AX108449.1 GI:13923775
KEYWORDS SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dorit,R.L. and Cole,K.B.
TITLE DNA-cleaving nuclease p rna
JOURNAL Patent: WO 0123548 A 12 05-APR-2001;
FEATURES Source 1..21
/organism="synthetic construct"
/db_xref="Taxon:32630"
/note="primer"

BASE COUNT 7 a 10 g 3 t
ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 21 CTTTCACCT 12

RESULT 8
AX108450
LOCUS AX108450
DEFINITION Sequence 13 from Patent WO0123548.
ACCESSION AX108450
VERSION AX108450.1 GI:13923776
KEYWORDS SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dorit,R.L. and Cole,K.B.
TITLE DNA-cleaving nuclease p rna
JOURNAL Patent: WO 0123548 A 13 05-APR-2001;
FEATURES Source 1..21
/organism="synthetic construct"
/db_xref="Taxon:32630"
/note="Synthetic primer"

BASE COUNT 4 a 6 c 4 g 5 t
ORIGIN 1 CTTTCACCT 10
/db_xref="Taxon:32630"
/note="primer"

Query Match 100.0%; Score 10; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 7 CTTTCACCT 16

RESULT 7
AX108449
LOCUS AX108449
DEFINITION Sequence 21 from Patent EP1197495.
ACCESSION AX108449
VERSION AX108449.1 GI:21522724
KEYWORDS SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Higashi,K. and Komatsu,K.
TITLE Dna-binding protein Yb-1-containing collagen accumulation
JOURNAL Patent: EP 1197495-A 21 17-APR-2002;
FEATURES source 1..21
/organism="synthetic construct"
/db_xref="Taxon:32630"
/note="Designed oligonucleotide primer to synthesize collagen alpha 1 probe"

BASE COUNT 6 a 4 c 8 g 3 t
ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 11 CTTTCACCT 2

RESULT 10
AX476918
LOCUS AX476918
DEFINITION Sequence 9 from Patent WO0220848.
ACCESSION AX476918
VERSION AX476918.1 GI:22216171
KEYWORDS SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P., Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
TITLE Gene and sequence variation associated with cancer
JOURNAL Patent: WO 0220848-A 9 14-MAR-2002;
FEATURES Source 1..21
/organism="synthetic construct"
/db_xref="Taxon:32630"
/note="Synthetic primer"

BASE COUNT 4 a 9 c 1 g 7 t
ORIGIN

Query Match	100.0%	Score 10; DB 6; Length 21;	PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00
Best Local Similarity	100.0%	Pred. No. 1.9e+05;	CC Description of Artificial Sequence: artificially synthesized
Matches	10;	Indels 0;	primer
Conservative	0;	Gaps 0;	
QY	1 CTTTCACCT 10		
Db	11 CTTTCACCT 20		
RESULT 11			
LOCUS	BD013048	21 bp	DNA linear
DEFINITION	Paranyxovirus having modified transcription initiation sequence.	PAT 02-AUG-2002	
ACCESSION	BD013048		
VERSION	BD013048.1	GI:22093237	
KEYWORDS	WO 0118223-A/11.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	NagaI, Y., Kato, A. and Hasegawa, M.		
TITLE	Paranyxovirus having modified transcription initiation sequence		
JOURNAL	Patent: WO 0118223-A 11 15-MAR-2001;		
DNA/VEC	RESEARCH INC. YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA		
OS	Artificial Sequence		
PN	WO 0118223-A/11		
PD	15-MAR-2001		
PR	06-SEP-2000	WO 20001P006051	
PI	YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA		
PC	C12N15/86,C12N15/45//A61K31/7105,A61K48/00		
CC	Description of Artificial Sequence; artificially synthesized		
primer			
CC	sequence		
CC	synthetic construct.		
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
QY	1 CTTTCACCT 10		
Db	9 CTTTCACCT 18		
RESULT 13			
ID	BD010081/C		
ACCESSION	BD010081	standard; DNA; SYN; 21 BP.	
AC	BD010081;		
XX			
SV	BD010081.1		
XX			
DT	08-FEB-2002 (Rel. 70, Created)		
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)		
XX			
DE	Paranyxovirus having modified transcription initiation sequence.		
XX			
KW	JP 03075813-T/11.		
XX			
OS	synthetic construct.		
OC	artificial sequence.		
XX			
RN	[1]		
RP	1-21		
RA	NagaI, Y., Kato, A., Hasegawa, M.		
RT	Paranyxovirus having modified transcription initiation sequence".		
RL	Patent number JP03075813-T/11, 06-MAR-2001.		
RL	DNA/VEC RESEARCH INC. YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.		
XX			
CC	OS		
CC	Artificial Sequence		
CC	PN		
CC	JP 03075813-T/11		
CC	PD		
CC	06-MAR-2001		
CC	06-SEP-2000	JP 2000006051	
CC	PR		
CC	06-SEP-1999	JP 99P 252231	
CC	PI		
CC	C12N15/86,C12N15/45//A61K31/7105,A61K48/00		
DEFINITION	Paranyxovirus having modified transcription initiation sequence.		
ACCESSION	BD013049		
VERSION	BD013049.1	GI:22093238	
KEYWORDS	WO 0118223-A/12.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	NagaI, Y., Kato, A. and Hasegawa, M.		
TITLE	Paranyxovirus having modified transcription initiation sequence		
JOURNAL	Patent: WO 0118223-A 12 15-MAR-2001;		
DNA/VEC	RESEARCH INC. YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA		
OS	Artificial Sequence		
PN	WO 0118223-A/12		
PD	15-MAR-2001		
PR	06-SEP-2000	WO 20001P006051	
PI	06-SEP-1999	JP 99P 252231	
YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA			
RESULT 12			
LOCUS	BD013049	21 bp	DNA linear
DEFINITION	Paranyxovirus having modified transcription initiation sequence.	PAT 02-AUG-2002	
ACCESSION	BD013049		
VERSION	BD013049.1	GI:22093238	
KEYWORDS	WO 0118223-A/12.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	NagaI, Y., Kato, A. and Hasegawa, M.		
TITLE	Paranyxovirus having modified transcription initiation sequence		
JOURNAL	Patent: WO 0118223-A 12 15-MAR-2001;		
DNA/VEC	RESEARCH INC. YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA		
OS	Artificial Sequence		
PN	WO 0118223-A/12		
PD	15-MAR-2001		
PR	06-SEP-2000	WO 20001P006051	
PI	06-SEP-1999	JP 99P 252231	
YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA			
FEATURES			
source			
FT			
FT			
FT			
XX			
SQ	Sequence 21 BP; 4 A; 4 C; 6 G; 7 T; 0 other;		
XX			
DE	Query Match 100.0%; Score 10; DB 23; Length 21;		
XX	Best Local Similarity 100.0%; Pred. No. 1.9e+05;		
DE	Mismatches 0; Indels 0; Gaps 0;		
XX	Comments 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CTTTCACCT 10		
XX			

Db 13 CTTTCACCT 4

source 1..22
/organism="unknown"
base count 6 a 6 c 5 g 5 t
origin

Query Match 100.0%; Score 10; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 10; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10
Db 10 CTTTCACCT 19

XX 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
DE Paramyxovirus having modified transcription initiation sequence.
KW JP 03075813-T/12.
XX OS synthetic construct.
OC artificial sequence.
XX
RN [1]
RP 1..21
RA Nagai Y., Kato A., Hasegawa M.;
RT "Paramyxovirus having modified transcription initiation sequence";
RL DNAVEC RESEARCH INC.YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.
XX
CC OS Artificial Sequence
CC PN JP 03075813-T/12
CC PD 06-MAR-2001
CC PP 06-SEP-1999 JP 99P 25231
CC PR 06-SEP-1999 JP 99P 25231
CC PI YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA
CC PC C12N15//86,C12N15//45//A61K31//7105,A61K48/00
CC
CC Key Location/Qualifiers
CC FT 1.. 21
CC FT /organism="Artificial Sequence"
XX
FH Key
FH FT source 1.. 21
FH FT /db_xref="taxon:32630"
FH FT /organism="synthetic construct"
XX
SQ Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 10; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
*
Qy 1 CTTTCACCT 10
||| |||||
Db 9 CTTTCACCT 18

RESULT 15

AR099567 AR099567 22 bp DNA linear PAT 14-FEB-2001

LOCUS AR099567 Sequence 94 from patent US 6077833.

DEFINITION Sequence 94 from patent US 6077833.

ACCESSION AR099567

VERSION AR099567.1 GI:12809333

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
PATENT: US 6077833-A 94 20-JUN-2000;
FEATURES Location/Qualifiers

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Run on:	March 18, 2003, 23:06:05 ; Search time 168 seconds (without alignments)			
Om nucleic - nucleic search, using sw model				
Title:	US - 09-702-498a-33			
Perfect score:	10			
Sequence:	1 CTTTCACCTT 10			
Scoring table:	IDENTITY.NUC			
Gapop:	10.0 , Gapext 1.0			
Searched:	2185239 seqs, 1125999159 residues			
Total number of hits satisfying chosen parameters:	4370478			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 45 summaries			
Database :				
	N_Genesed_101002:*			
1:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1980.DAT:*			
2:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1981.DAT:*			
3:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1982.DAT:*			
4:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1983.DAT:*			
5:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1984.DAT:*			
6:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1985.DAT:*			
7:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1986.DAT:*			
8:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1987.DAT:*			
9:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1988.DAT:*			
10:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1989.DAT:*			
11:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1990.DAT:*			
12:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1991.DAT:*			
13:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1992.DAT:*			
14:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1993.DAT:*			
15:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1994.DAT:*			
16:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1995.DAT:*			
17:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1996.DAT:*			
18:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1997.DAT:*			
19:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA1998.DAT:*			
20:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA2000.DAT:*			
21:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA2001A.DAT:*			
22:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA2001B.DAT:*			
23:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA2002.DAT:*			
24:	/SIDS2/gcdata/genesed/geneseq/geneseq-emb1/NA2002.DAT:*			
Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Query			
	Score			
	Match Length			
	DB ID			
	Description			
1	10.00.0	10 22	AAH65896	Nucleotide sequence
2	10.00.0	10 22	AAH73613	DNA sequence, SEQ
3	10.00.0	10 22	AHH2653	S sequence oligonucleotide
4	10.00.0	10 22	AHF86115	Sendai virus S seq
5	10.00.0	10 22	AHF77598	Modified transcript
6	10.00.0	10 24	AHL47265	Sendai virus S seq
7	10.00.0	10 24	AHL38107	Angiogenesis gene
8	10.00.0	10 24	ABK48812	DNA sequence #1 re
9	10.00.0	10 24	ABL39904	Sendai virus S oligo
ALIGNMENTS				
RESULT 1				
ID	AA165896			
XX	standard; DNA; 10 BP.			
XX	AA165896;			
AC				
XX				
DT	03-JAN-2002 (first entry)			
XX				
DE	Nucleotide sequence of a synthetic oligonucleotide.			
XX				
Vaccine; Sendai virus vector; viral protein; immunodeficiency virus; AIDS; antigen gene; nasal mucosa; lymph node; ss.				
XX				
OS	Synthetic.			
XX				
XX	WO200172340-A1.			
PD	04-OCT-2001.			
XX				
PP	30-MAR-2001; 2001WO-JP02769.			
XX				
PR	30-MAR-2000; 2000US-193127P.			
XX				
PA	(D NAV-) DN AVEC RES INC.			
PA	(NINA) JAPAN NAT INST INFECTIOUS DISEASES.			
XX				
PL	Kano M, Matano T, Kato A, Nagai Y, Hasegawa M;			
XX				
DR	WPI; 2001-616443/71.			
XX				
PT	Viral protein of immunodeficiency virus-encoding Sendai virus			
PT	vector-based AIDS virus vaccine for provision of efficient protective			

XX
 PT immunity comprises nasal administration to e.g. macaque to suppress
 XX onset and progress of AIDS -

PS Disclosure; Page 27; 92pp; Japanese.

XX
 CC The specification describes a vaccine containing a Sendai virus vector
 CC which encodes the viral protein of immunodeficiency virus. The vaccine
 CC is for treating AIDS, with expression of antigen gene mediated by the
 CC vector in nasal mucosa and local lymph nodes detected and
 CC antigen-specific cell-mediated response induced at significant
 CC level after vaccination. The present sequence represents an
 CC oligonucleotide which is used in the course of the invention.

XX
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query	100.0%	Score	10	DB	22	Length	10
Best Local Similarity	100.0%	Pred. No.	4	2e+03			
Matches	10	Conservative	0	Mismatches	0	Indels	0
Qy	1 CTTTCACCC T 10						
Db	1 CTTTCACCC T 10						

XX
 RESULT 2
 AAH73613 AAH73613 standard; DNA; 10 BP.

XX
 AC AAH73613;

XX
 DT 27-SEP-2001 (first entry)

XX
 DE DNA sequence, SEQ ID NO: 1.

XX
 KW Gene therapy; vascular disorder; recombinant paramyxovirus vector; ds.

XX
 OS Unidentified.

XX
 PN WO200153491-A1.

XX
 PD 26-JUL-2001.

XX
 PF 11-JAN-2001; 2001W0-JP00087.

XX
 PR 19-JAN-2000; 2000JP-0014136.

XX
 PA (DNAV-) DNAVEC RES INC.

XX
 PI Masaki I, Yonemitsu Y, Sueishi K, Hasegawa M, Kinoh H;

XX DR WPI; 2001-45610/49.

XX
 PT Paramyxovirus vector containing foreign gene for efficient gene
 PT transfer into vascular cells

XX
 PS Disclosure; Page 19; 84pp; Japanese.

XX
 CC The invention relates to a method for inserting nucleic acid into blood
 CC vessel cells by contacting the cells with the nucleic acid contained in
 recombinant paramyxovirus vector or cells transformed by it. The
 CC method can be used for gene therapy of vascular disorders. Genes that
 CC can be introduced into blood vessel cells by this method include cell
 cycle regulators (such as p53, p21, p16 and p27), inhibitory factors
 CC (such as H-Ras, eNOS and C-natriuretic peptide), ion channels (such as
 CC Kir 6.2, potassium channel), blood proteins (such as urokinase and
 CC tissue plasminogen activator), tissue factor pathway inhibitors (such
 CC as tPP1) and vascular growth factors (such as vascular endothelial
 CC growth factor (VEGF), fibroblast growth factor (FGF) and hepatocyte
 CC growth factor (HGF)). The present sequence is provided in the
 CC specification.

XX
 Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query	100.0%	Score	10	DB	22	Length	10
Best Local Similarity	100.0%	Pred. No.	4	2e+03			
Matches	10	Conservative	0	Mismatches	0	Indels	0
Qy	1 CTTTCACCC T 10						
Db	1 CTTTCACCC T 10						

XX
 PS

Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCACCC 10
 Db 1 CTTTCACCC 10

RESULT 3
 AAH23653
 ID AAH23653 standard; DNA; 10 BP.
 XX
 AC AAH23653;
 XX
 DT 07-AUG-2001 (first entry)
 XX
 DE S sequence oligonucleotide used in a recombinant Sendai virus vector.
 XX
 KW Gene therapy; S sequence; airway epithelium; cystic fibrosis; ds.
 XX
 OS Parainfluenza virus.

XX
 KW Extracellular superoxide dismutase; EC-SOD; immunosuppressive;
 KW antiinflammatory; antiarthritis; antirheumatic; arthritis; colitis;
 KW systemic autoimmune disease; systemic lupus erythematosus;
 KW rheumatic myocarditis; progressive systemic sclerosis; dermatomyositis;
 KW Sjogren's syndrome; polyarteritis; Sendai virus; ss.
 OS Parainfluenza virus.
 XX CA2316518-A1.
 PN
 XX
 XX
 XX
 PD 01-MAR-2001.
 XX
 XX
 XX
 PR 31-AUG-2000; 2000CA-2316518.
 XX
 XX
 PR 01-SEP-1990; 99JP-0248032.
 PR 27-APR-2000; 2000CA-2304453.
 XX
 PA (DNAV-) DNA VEC RES INC.
 XX
 PA Yamauchi N, Fukumura M, Iyama S, Hasegawa M, Nitsu Y;
 DR WPI; 2001-300717/32.
 XX
 PT New EC-SOD Proteins and nucleic acids encoding the protein useful in
 PT gene therapy for treating or preventing systemic autoimmune diseases,
 e.g. rheumatoid arthritis, colitis and systemic lupus erythematosus.
 XX
 PS Disclosure: Page 24; 71PP; English.
 XX
 CC This invention relates to a superoxide dismutase (SOD) protein which
 CC exists extracellularly and is termed EC-SOD, and the polynucleotide
 CC encoding it. SOD is the enzyme that catalyses the reaction involved in
 CC superoxide anion radical production. The invention includes a vector
 CC containing the EC-SOD coding sequence, and a method for treating or
 CC preventing systemic autoimmune diseases comprising administering the
 CC vector. Methods using the EC-SOD protein and DNA sequences result in
 CC immunosuppressive, anti-inflammatory, antiarthritic, and antirheumatic
 CC activity. The EC-SOD protein and nucleic acid encoding the protein are
 CC useful for treating systemic autoimmune diseases such as arthritis,
 CC rheumatoid arthritis, colitis, systemic lupus erythematosus, rheumatic
 CC myocarditis, progressive systemic sclerosis, dermatomyositis, polymyositis,
 CC mixed connective tissue disease, Sjogren's syndrome, Polyarteritis, Wegener's
 CC granulomatosis and colitis. The present sequence represents a Sendai virus (Parainfluenza virus) oligonucleotide
 CC which can be used in the construction of a vector containing the EC-SOD
 CC gene.
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
 Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCACCT 10
 DB 1 CTTTCACCT 10
 DE Sendai virus S sequence complement.
 RESULT 6
 ID AAL47265
 ID AAL47265 standard; DNA; 10 BP.
 XX
 AC AAL47265;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Sendai virus vector; gene therapy; antiinflammatory; inflammation;
 KW cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis;
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;
 KW neuroprotective; immunosuppressive; antidiabetic; antirheumatic;
 KW transplant rejection; diabetes; chronic articular rheumatism;
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;
 KW iritis; granulomatous disease; chronic nephritis; scleroderma;
 KW hysteroscopic; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.
 OS Sendai virus.
 XX
 PN WO200238726-A2.
 XX
 PD 16-MAY-2002.
 XX
 AC
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Modified transcription initiation site Paramyxovirus related oligo #18.
 KW Transcription initiation sequence; viral vector; vaccine; therapy; ds.
 OS Unidentified.
 XX
 PN
 XX
 XX
 PR 06-SEP-1999; 99JP-0252231.
 PA (DNAV-) DNA VEC RES INC.
 XX
 PI Nagai Y, Kato A, Hasegawa M;
 XX
 DR WPI; 2001-244575/25.
 XX
 PT Paramyxovirus vectors with modified transcription initiation sequences
 PT for increased expression of foreign genes in production of drugs and
 PT vaccines.
 XX
 PS Disclosure: Page 17; 65pp; Japanese.
 XX
 CC The present invention describes a paramyxovirus vector DNA in which the
 CC transcription initiation sequence has been modified to modify the
 CC expression of a gene located downstream of the transcription initiation
 CC sequence. This is useful in the production of mutant paramyxovirus
 CC vectors with elevated gene expression and a more rapid proliferation than
 CC the wild-type vector, which can then be used for more efficient
 CC production of drug substances and vaccines.
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
 Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCACCT 10
 DB 1 CTTTCACCT 10
 DE Sendai virus S sequence complement.
 RESULT 6
 ID AAL47265
 ID AAL47265 standard; DNA; 10 BP.
 XX
 AC AAL47265;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Sendai virus vector; gene therapy; antiinflammatory; inflammation;
 KW cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis;
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;
 KW neuroprotective; immunosuppressive; antidiabetic; antirheumatic;
 KW transplant rejection; diabetes; chronic articular rheumatism;
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;
 KW iritis; granulomatous disease; chronic nephritis; scleroderma;
 KW hysteroscopic; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.
 OS Sendai virus.
 XX
 PN WO200238726-A2.
 XX
 PD 16-MAY-2002.
 XX
 PR 08-NOV-2001; 2001WO-JP09786.
 XX
 PR 08-NOV-2000; 2000JP-0339942.
 XX
 PA (DNAV-) DNA VEC RES INC.
 XX
 PI Griesenbach U, Ferrari S, Geddes DM, Alton EW, Hasegawa M, Hou X;
 XX
 DR WPI; 2002-490069/52.

XX
PT Novel paramyxovirus vector for gene transfer to cardiovascular system, in which expression product of gene comprised in vector is transferred to a site different from the site of administration through the bloodstream -
XX
PS Disclosure; Page 17; 67pp; English.

CC The present invention relates to a paramyxovirus vector for gene transfer to the cardiovascular system, where the expression product of a gene comprised in the vector is transferred to a site different from the site of administration through the bloodstream. The vector is useful for transferring sequences such as IL-10 to the cardiovascular system, for treating pneumonia in cystic fibrosis patients and for treating inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis, prostatomegaly, multiple sclerosis, post transplant rejection, diabetes, chronic articular rheumatism, psoriasis, inflammatory enteropathy, systemic lupus erythematosus, iritis, granulomatous disease, chronic nephritis, scleroderma, heterotonia, keloid and cirrhosis. The present sequence is a DNA fragment used to produce the vector of the invention.

XX
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10
Db 1 CTTTCACCT 10

RESULT 7
ID AAL38107 standard; DNA; 10 BP.

XX
AC AAL38107;
XX
DT 15-AUG-2002 (first entry)

XX
DE Angiogenesis gene containing paramyxovirus vector related oligo #1.

XX
KW Vasotropic; paramyxovirus vector; angiogenesis gene; gene therapy; FGF2; ischaemia; virus vector; edema; tissue targeting; ds.

XX
OS Unidentified.

XX
PN WO200242481-A1.

XX
PD 18-APR-2002.

XX
PF 26-SEP-2001; 2001WO-JP08372.

XX
PR 06-OCT-2000; 2000JP-0308533.

XX
PA (INAV-) DNAVEC RES INC.

XX
PI Hukumura M, Shiotani A, Maeda M, Hasegawa M;

XX
DR WPI; 2002-340180/37.

XX
PT Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders

XX
PS Disclosure; Page 14; 56pp; Japanese.

CC The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after injection and is safe, non-infective and does not cause tumorigenesis. The present DNA sequence of unknown function is given in the specification or the present invention.

XX
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10
Db 1 CTTTCACCT 10

RESULT 8
ID ABL48812
XX
AC ABL48812;
XX
DT 15-JUL-2002 (first entry)

XX
DE DNA sequence #1 relating to paramyxovirus vector for gene transfer.

XX
KW Method for gene transfer; skeletal muscle; paramyxovirus vector; gene therapy; neuromuscular disorder; tumorigenesis; neuroprotective; myotrophic; insulin-like growth factor; IGF; ds.

XX
OS Unidentified.

XX
PN WO200231138-A1.

XX
PD 18-APR-2002.

XX
PF 26-SEP-2001; 2001WO-JP08372.

XX
PR 06-OCT-2000; 2000JP-0308533.

XX
PA (INAV-) DNAVEC RES INC.

XX
PI Hukumura M, Shiotani A, Maeda M, Hasegawa M;

XX
DR WPI; 2002-340180/37.

XX
PT Paramyxovirus vector for transferring foreign gene e.g. insulin-like growth factor into skeletal muscle in gene therapy of neuromuscular disorders

XX
PS Disclosure; Page 14; 56pp; Japanese.

CC The present invention relates to a method for transferring a foreign gene into skeletal muscle. The method comprises administering a paramyxovirus inserted with the foreign gene. The paramyxovirus vector is useful for transferring a foreign gene e.g. insulin-like growth factor (IGF) into skeletal muscle in the gene therapy of neuromuscular disorders. Such a vector can sustain transgene expression for up to a month after injection and is safe, non-infective and does not cause tumorigenesis. The present DNA sequence of unknown function is given in the specification or the present invention.

XX
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10
Db 1 CTTTCACCT 10

RESULT 9
ID ABL39904
XX
ID ABL39904 standard; DNA; 10 BP.

XX
CC The invention relates to a paramyxovirus vector containing an angiogenesis gene, which can be used for gene therapy of ischaemia in tissues including brain, heart, lung, skeletal muscle and kidney. The expression of the virus vector is free from edema and specific tissues can be targeted. This polynucleotide sequence represents an artificial oligonucleotide relating to the paramyxovirus vector containing an angiogenesis gene FGF2 of the invention.

CC

AC ABL39904;
 XX (first entry)
 DT 14-MAY-2002
 XX
 DE Sendai virus S oligonucleotide SEQ ID NO:1.
 XX
 KW Sendai virus; virus vector; renal cell; paramyxovirus; gene transfer;
 KW gene therapy; kidney; nephrotropic; antidiabetic; diabetes; renopathy;
 KW chronic glomerulonephritis; glomerulosclerosis; Alport's syndrome;
 KW tubulointerstitial nephritis; ss.
 XX
 OS Parainfluenza virus.
 XX
 PN WO200200264-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-JP05513.
 XX
 PR 27-JUN-2000; 2000JP-0197870.
 PA
 XX
 PI Imai E, Isaka Y, Fukumura M, Hasegawa M;
 DR WPI; 2002-130841/17.
 XX
 PS
 PT Transferring a gene into renal cells, useful for gene therapy of a
 PT kidney to treat e.g. chronic glomerulonephritis, comprises using a
 virus vector, particularly of paramyxovirus
 XX
 PS Example 1, Page 38; 75pp; Japanese.
 XX
 CC The present invention describes transferring a gene into renal cells
 CC comprising contacting a paramyxovirus vector with the renal cells,
 CC particularly by administration into blood vessels, especially the renal
 CC artery or into the urethra. Also described are: (1) a paramyxovirus
 CC vector for use in transferring a gene into renal cells; and
 CC (2) compositions for transferring a gene into renal cells comprising
 CC cells having the paramyxovirus vector or the vector. The method is used
 CC for transferring a gene into renal cells. The virus is applicable in
 CC gene therapy for the kidney to treat target diseases of e.g. chronic
 CC glomerulonephritis, diabetes, nephropathy, glomerulosclerosis,
 CC tubulointerstitial nephritis and Alport's syndrome. The transfer of a
 CC gene into renal cells is with high efficiency, and after brief exposure,
 CC the transferred gene is continuously expressed in renal cells over a
 CC long period of time. The present sequence represents a Sendai virus
 CC (parainfluenza virus) oligonucleotide which is used in an example from
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
 Query Match 100.0%; Score 10; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4_3e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTTCACCC 10
 Db 1 CTTTCACCC 10
 RESULT 11
 AR18122;C
 ID AR18122
 XX
 AC AR18122;
 XX
 DT 22-AUG-1996 (first entry)
 DE Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).
 XX
 KW Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;
 KW PCR amplification of specific alleles; PASA; compulsive disorder;
 KW cocaine dependence; alcoholism; genetic susceptibility; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key allele 6
 FT Location/Qualifiers
 FT /*tag= a
 FT /*note= "nucleotides 3203-3213 of DRD2 in which
 FT there is a T at the polymorphic position
 XX
 PN US5500343-A.
 XX

PD 19-MAR-1996.
 XX
 PR 07-FEB-1990; 90US-0477057.
 XX
 PR 24-JUN-1992; 92US-0903183.
 XX
 PR 07-FEB-1990; 90US-0477057.
 XX
 PR 23-JAN-1992; 92US-0826222.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Blum K, Noble EP, Sheridan PJ;
 XX
 DR WPI; 1996-171043/17.
 XX
 PT Detecting genetic potential susceptibility to cocaine dependence or alcoholism - by detecting human dopamine-D2 receptor gene A1 or B1 allele in the subject's DNA
 PT
 PS Example 3; Column 45; 56pp; English.
 XX
 The dopamine D2 receptor DRD2(1n6-Bx7) haplotype is comprised of two polymorphisms that are separated by 212 bp and span the junction of the intron 6 and exon 7 sequences. The first is a T or C at position 3208 and the second polymorphism is a T or C at position 3420, providing 4 possible haplotypes. Haplotype I is characterised by T at position 3208 and C at position 3420. The Primers #3208 and #3420 specifically amplify a 241 bp fragment (3433-3195+1) beginning in intron 6 and ending in exon 7 of the dopamine D2 receptor haplotype I which is associated with alcoholism. The primers are used in a claimed method for detecting genetic potential susceptibility to alcoholism in human subjects. In particular, amplification is carried out using the PASA technique (i.e. PCR amplification of Specific Alleles). In related methods, genetic potential susceptibility to cocaine dependence can be detected by amplifying human dopamine D2 receptor A1 and B1 alleles (primers not specified).
 XX
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;
 Query Match 100 %; Score 10; DB 17; Length 11;
 Best Local Similarity 100 %; Pred. No. 4.3e+03;
 Matches 10; Conservative 0; Mismatches 0; Indexs 0; Gaps 0;
 QY 1 CTTTCACCCCT 10
 Db 11 CTTTCACCCCT 2
 RESULT 12
 AAX14846/C
 ID AAX14846 standard; DNA; 12 BP.
 AC AAX14846;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE triple helix forming nucleotides 384-395 of 23S rRNA gene.
 KW Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
 KW Leptospira interrogans.
 OS
 PN US5861244-A.
 XX
 PD 19-JAN-1999.
 XX
 PR 22-DEC-1993; 93US-0173489.
 XX
 PR 22-DEC-1993; 93US-0173489.
 PR 29-OCT-1992; 92US-0968436.
 XX
 PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
 XX
 PI Hepburn AG, Wang C;
 XX
 DR WPI; 1999-130384/11.
 XX
 PT Assay of genetic sequences based on triplex formation from double stranded analytic - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria
 PT
 PS Disclosure; Columns 21-22; 168pp; English.
 XX
 CC The present sequence represents a potential triple-helix forming region.
 CC It can be used to demonstrate the assay of the invention. The assay
 CC comprises adding a sample containing double stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA, which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.
 XX
 SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 other;
 Query Match 100 %; Score 10; DB 20; Length 12;
 Best Local Similarity 100 %; Pred. No. 4.3e+03;
 Matches 10; Conservative 0; Mismatches 0; Indexs 0; Gaps 0;
 QY 1 CTTTCACCCCT 10
 Db 12 CTTTCACCCCT 3
 RESULT 13
 ABF08726/C
 ID ABF08726 standard; DNA; 13 BP.
 XX
 AC ABF08726;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic; Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001..
 XX
 PR 06-APR-2001; 2001WO-1B00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
 XX
 PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.

```

Query Match          100.0%;  Score 10;  DB 23;  Length 13;
Best Local Similarity 100.0%;  Pred. No. 4.3e+03;  Mismatches 0;
Matches 10;  Conservative 0;  Indels 0;  Gaps 0;
OY
  1 CTTTCACCC 10
Db
  1 CTTTCACCC 10

RESULT 15
ABH4716rc

```

Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other; ID ABH24716 standard; DNA; 13 BP.
 Query Match 100 %; Score 10; DB 23; Length 13; XX
 Best Local Similarity 100.0%; Pred. No. 4.3e+03; AC
 Matches 10; Conservative 0; Mismatches 0; Indels XX
 Qy 1 CTTTCACCC 10 ABH24716;
 Db 13 CTTTCACCC 4 DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 224693 for detecting SNP TSC0054769.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer

RESULT 14
 ABF08727
 ABF08727 standard; DNA; 13 BP.
 ID
 XX
 AC
 XX
 ABF08727;
 XX
 DT
 21-FEB-2002 (first entry)
 XX
 DE
 Oligonucleotide SEQ ID NO 108724 for detecting SNP TSC0027206.
 XX
 XX
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-1B00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status;
 XX
 PD 18-OCT-2001.
 XX
 WO200177384-A2.
 XX

XX 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIC-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single nucleotide polymorphisms and cytosine
 methylation status -
 XX Claim 1; SEQ ID 108724; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;
 CC Query Match 100.0%; Score 10; DB 23; Length 13;
 CC Best Local Similarity 100.0%; Prd. No. 4.3e+03;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC AB00010-ABC9989, ABF00010-ABF9989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

Wed Mar 19 09:04:46 2003

us-09-702-498a-33.rng

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Om nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:00:11; Search time 37 seconds

(without alignments)
 82.1886 Million cell updates/sec

Title: US-09-702-498a-33
 Perfect score: 10
 Sequence: CTTTCACCT 10.

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA: *
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
 5: /cgn2_6/ptodata/1/ina/PCTRUS.COM.seq: *
 6: /cgn2_6/ptodata/1/ina/bacfile1.seq: *

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	10	100.0	111	1	US-07-909-383-1
C 2	10	100.0	112	2	US-08-173-439CC-233
C 3	10	100.0	119	3	US-08-177-266A-95
C 4	10	100.0	119	4	US-09-326-186B-95
C 5	10	100.0	222	3	US-08-777-266A-94
C 6	10	100.0	222	4	US-08-326-186B-94
C 7	10	100.0	231	1	US-07-952-442-7
C 8	10	100.0	231	1	US-08-269-66-7
C 9	10	100.0	231	1	US-08-319-545A-7
C 10	10	100.0	232	2	US-09-092-988-7
C 11	10	100.0	233	3	US-09-129-034-7
C 12	10	100.0	234	4	US-09-777-266A-93
C 13	10	100.0	244	3	US-08-326-186B-93
C 14	10	100.0	244	4	US-09-326-186B-93
C 15	10	100.0	124	4	US-08-205-697A-39
C 16	10	100.0	124	5	US-08-702-525-39
C 17	10	100.0	124	5	PCT-US5-0276-39
C 18	10	100.0	333	3	US-09-009-913-15
C 19	10	100.0	377	2	US-09-702-652-40
C 20	10	100.0	377	6	5168053-1
C 21	10	100.0	397	2	US-09-636-597-2
C 22	10	100.0	397	4	US-09-232-063-2
C 23	10	100.0	438	4	US-09-228-565-56
C 24	10	100.0	440	4	US-09-397-867-321
C 25	10	100.0	584	4	US-09-328-111-83
C 26	10	100.0	616	4	US-09-328-111-574
C 27	10	100.0	650	4	US-09-328-111-189

RESULT 1
 US-07-909-383-1/C
 Sequence 1, Application US/07909383
 Patent No. 5500343

GENERAL INFORMATION:

APPLICANT: NOBLE, E. P.
 APPLICANT: BLUM, KENNETH
 APPLICANT: SHERIDAN, P.J.
 TITLE OF INVENTION: ALLElic ASSOCIATION OF THE HUMAN
 TITLE OF INVENTION: DOPAMINE (D2) RECEPTOR GENE IN
 TITLE OF INVENTION: COMPULSIVE DISORDERS
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/909,383
 FILING DATE: 19930624
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HODGINS, DANIEL S.
 REGISTRATION NUMBER: 31,025
 REFERENCE/DOCKET NUMBER: US/3K:187

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-320-7200
 TELEFAX: 512-474-7577
 TELEX: NOT APPLICABLE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 base Pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0; Sequence 2, Appl1 Sequence 56, Appl1 Sequence 39, Appl1 Sequence 15, Appl1 Sequence 40, Appl1 Sequence 574, Appl1 Sequence 189, Appl1

Db 11 CTTTCACCC 2

Db

RESULT 2 US-08-173-489C-233/C

; Sequence 233, Application US/08173489C

; Patent No. 5861244

; GENERAL INFORMATION:

; APPLICANT: HEPBURN, A. G.

; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA

; NUMBER OF SEQUENCES: 365

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

; STREET: 510 EAST 73RD STREET,

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10021.

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44MB storage

; COMPUTER: IBM PC/XT/AT

; OPERATING SYSTEM: MS-DOS version 5.2

; SOFTWARE: WordPerfect Version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/173,489C

; FILING DATE: 22 DEC 1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/968,436

; FILING DATE: 29 OCT 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Handelman, Joseph H.

; REGISTRATION NUMBER: 26,179

; REFERENCE/DOCKET NUMBER: U9518-6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (attorney) (212) 708-1880

; TELEFAX: (attorney) (212) 246-8959

; INFORMATION FOR SEQ ID NO: 233:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; DESCRIPTION: 23S rRNA gene from Leptospira

; DESCRIPTION: Interrogans (Accession # X14249) nucleotides

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Leptospira interrogans serovar canicola

; STRAIN: moulton

; PUBLICATION INFORMATION:

; AUTHORS: Fukunga, M, Horie, I, Mifuchi, T.

; TITLE: Nucleotide sequence of a 23S

; TITLE: ribosomal RNA gene for Leptospira interrogans

; JOURNAL: serovar canicola strain moulton

; VOLUME: 17

; PAGES: 2123-2123

; DATE: 1989

; RELEVANT RESIDUES IN SEQ ID NO: 233 :FROM 1 TO 12

; US-08-173-489C-233

; Query Match 100.0%; Score 10; DB 2; Length 12;

; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0;

; Matches 10; Conservative 0; Indels 0; Gaps 0;

; Qy 1 CTTTCACCC 10

; Db 12 CTTTCACCC 3

RESULT 3 US-08-77-266A-95

; Sequence 95, Application US/0877266A

; Patent No. 6077833

; GENERAL INFORMATION:

; APPLICANT: Clarence Frank Bennett

; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Expression of B7 Protein

; NUMBER OF SEQUENCES: 125

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Jane Massey Licata

; STREET: 210 Lake Drive East, Suite 201

; CITY: Cherry Hill

; STATE: NJ USA

; COUNTRY: USA

; ZIP: 08002

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/777,266A

; FILING DATE: December 31, 1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane Massey Licata

; REGISTRATION NUMBER: 32,257

; REFERENCE/DOCKET NUMBER: ISPH-0201

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (609) 779-2400

; TELEFAX: (609) 779-8488

; INFORMATION FOR SEQ ID NO: 95:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; ANTI-SENSE: Yes

; US-08-77-266A-95

; Query Match 100.0%; Score 10; DB 3; Length 19;

; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Mismatches 0;

; Matches 10; Conservative 0; Indels 0; Gaps 0;

; Qy 1 CTTTCACCC 10

; Db 7 CTTTCACCT 16

; RESULT 4 US-09-326-186B-95

; Sequence 95, Application US/09326186B

; Patent No. 6319906

; GENERAL INFORMATION:

; APPLICANT: Bennett, Clarence Frank

; TITLE: Vickers, Timothy A.

; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Expression of B7 Protein

; TITLE OF INVENTION: Modulation of the Expression of B7 Protein

; FILE REFERENCE: ISPH-0376

; CURRENT APPLICATION NUMBER: US/09/326,186B

; CURRENT FILING DATE: 1999-06-04

; PRIOR APPLICATION NUMBER: 08/777,266

; PRIOR FILING DATE: 1996-12-31

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 95

LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-09-326-186B-95

Query Match 100.0%; Score 10; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGACCT 10
 Db 7 CTTGACCT 16

RESULT 5
 US-08-777-266A-94
 Sequence 94, Application US/08777266A
 Patent No. 6077833

GENERAL INFORMATION:
 APPLICANT: Clarence Frank Bennett
 APPLICANT: Timothy A. Vickers
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
 Modulation of the Expression of B7 Proteins
 TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
 NUMBER OF SEQUENCES: 125
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Jane Massey Licata
 STREET: 2110 Lake Drive East, Suite 201
 CITY: Cherry Hill
 STATE: NJ
 COUNTRY: USA
 ZIP: 08002

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-777-266A
 FILING DATE: December 31, 1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 32,257
 REFERENCE/DOCKET NUMBER: ISP-H-0201
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 779-2400
 TELEFAX: (609) 779-8488
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 ANTI-SENSE: Yes
 US-08-777-266A-94

Query Match 100.0%; Score 10; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGACCT 10
 Db 10 CTTGACCT 19

RESULT 5
 US-08-777-266A-94
 Sequence 94, Application US/08777266A
 Patent No. 6319906
 GENERAL INFORMATION:
 APPLICANT: Bennett, Clarence Frank
 APPLICANT: Vickers, Timothy A.
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
 Modulation of the Expression of B7 Proteins
 FILE REFERENCE: ISPH-0376
 CURRENT APPLICATION NUMBER: US/09/326,186B
 CURRENT FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 08/777,266
 PRIOR FILING DATE: 1996-12-31
 NUMBER OF SEQ ID NOS: 226
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 94
 LENGTH: 22

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 ; US-09-326-186B-94

Query Match 100.0%; Score 10; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGACCT 10
 Db 10 CTTGACCT 19

RESULT 7
 US-07-952-442-7
 Sequence 7, Application US/07952442
 Patent No. 5574525

GENERAL INFORMATION:
 APPLICANT: Lalouel, Jean-Marc
 APPLICANT: Jeunemaître, Xavier
 APPLICANT: Linton, Richard P.
 APPLICANT: Soubré, Florent
 APPLICANT: Korelevsev, Youri
 APPLICANT: Corval, Pierre
 TITLE OF INVENTION: Angiotensinogen Gene Variants and
 TITLE OF INVENTION: Predisposition to Essential Hypertension
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,442
 FILING DATE: 19920930
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Innen, Jeffrey L.
 REGISTRATION NUMBER: 28,937
 INFORMATION FOR SEQ ID NO: 7:
 REFERENCE/DOCKET NUMBER: 19780-104502
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEPHONE: 202-962-4300
 TELEPHONE: 202-962-4300
 LENGTH: 23 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

RESULT 6
 US-09-326-186B-94
 Sequence 94, Application US/09326186B

APPLICANT: Kotolevtsiev, Youri
 APPLICANT: Cottvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 TITLE OF INVENTION: to Hypertension
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: D.C.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1/5.2 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/092,988
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/319,545
 ATTORNEY/AGENT INFORMATION:
 FILING DATE:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 19780-104502-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-092-988-7

Query Match 100.0%; Score 10; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCACCT 10
 Db 13 CTTTCACCT 22

RESULT 11
 US-09-106-216-7
 ; Sequence 7, Application US/09106216
 ; Patent No. 6153386
 ; General Information:
 APPLICANT: Lalouel, Jean-Marc
 APPLICANT: Jeunemaitre, Xavier
 APPLICANT: Lofton, Richard P.
 APPLICANT: Soubrier, Florent
 APPLICANT: Kotolevtsiev, Youri
 APPLICANT: Cottvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rothwell, Figg, Ernst & Kurz
 STREET: 555 Thirteenth Street N.W., Suite 701-E
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/106,216
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/106/498
 FILING DATE: 08-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/319,545
 FILING DATE: 07-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/952,545
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 2323-124
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-783-6040
 TELEFAX: 202-783-6031
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "primer"
 US-09-106-216-7

Query Match 100.0%; Score 10; DB 3; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCACCT 10
 Db 13 CTTTCACCT 22

RESULT 12
 US-09-429-034-7
 ; Sequence 7, Application US/09429034
 ; Patent No. 6165727
 ; General Information:
 APPLICANT: Lalouel, Jean-Marc
 APPLICANT: Jeunemaitre, Xavier
 APPLICANT: Lofton, Richard P.
 APPLICANT: Soubrier, Florent
 APPLICANT: Kotolevtsiev, Youri
 APPLICANT: Cottvol, Pierre
 TITLE OF INVENTION: Method to Determine Predisposition
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: D.C.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1/5.2 Windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/429,034
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/319,545
 FILING DATE: 7-OCT-1994
 APPLICATION NUMBER: US 07/952,442
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
 ATTORNEY/AGENT NUMBER: 28, 957
 REFERENCE/DOCKET NUMBER: 19780-104502-2
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810
 TELEFAX: (609) 779-2400
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens

US-09-429-034-7

RESULT 13

Query Match 100.0%; Score 10; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6 2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CTTTCACCT 10
Db	13 CTTTCACCT 22

US-08-777-266A-93

Sequence 93, Application US/08777266A
 Patent No. 607833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett
 APPLICANT: Timothy A. Vickers
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata
 STREET: 210 Lake Drive East, Suite 201
 CITY: Cherry Hill
 STATE: NJ
 COUNTRY: USA
 ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777-266A
 FILING DATE: December 31, 1996
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 32, 257
 REFERENCE/DOCKET NUMBER: ISPH-0201
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 779-8488
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24

RESULT 14

Query Match 100.0%; Score 10; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6 2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CTTTCACCT 10
Db	12 CTTTCACCT 21

US-09-326-186B-93

Sequence 93, Application US/09326186B
 Patent No. 631906

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank
 APPLICANT: Vickers, Timothy A.

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Protein

FILE REFERENCE: ISPH-036
 CURRENT APPLICATION NUMBER: US/09/326,186B
 CURRENT FILING DATE: 1999-06-04
 PRIOR APPLICATION NUMBER: 08777,266
 PRIOR FILING DATE: 1996-12-31
 NUMBER OF SEQ ID NOS: 226
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 93

LENGTH: 24

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic

US-09-326-186B-93

RESULT 15

Query Match 100.0%; Score 10; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6 2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CTTTCACCT 10
Db	12 CTTTCACCT 21

US-08-205-697A-39/C

Sequence 39, Application US/08205697A
 Patent No. 6218510

GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.
 APPLICANT: Borrelli, Francescopaolo
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules and Uses Therefor

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: LATIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandravouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..124
US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTACCCCT 10
||| | | | |
Db 13 CTTTCACCT 4

Search completed: March 19, 2003, 01:26:20
Job time : 39 secs

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GenCore version 5.1.4-p5_4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:40:46 ; Search time 51.5 seconds
 (without alignments)
 136 t284 Million cell updates/sec

Title: US-09-702-498a-33
 Perfect score: 10
 Sequence: 1 CTTCACCC 10

Scoring table: IDENTITY_NUC
 Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 1002604
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0% .
 Maximum Match 100% .
 Listing first 45 summaries

Database : Published_Applications_NA:*

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2: /cgn2_6/ptodata/1/pubnra/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubnra/NS05_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubnra/NS06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubnra/NS07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubnra/NS08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubnra/NS08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubnra/NS08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubnra/NS09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubnra/NS09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubnra/NS10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubnra/NS10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubnra/NS60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubnra/NS60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

US-09-966-277-63

Sequence 63, Application US/09966277

Patent No: US20020169306A1

GENERAL INFORMATION:

APPLICANT: KITAZATO, Kaio
 SHU, Tsugunire
 KUMA, Hidekazu

APPLICANT: UEDA, Yasuji

APPLICANT: ASAKAWA, Makoto
 HASEGAWA, Mamoru

APPLICANT: ITIDA, Akihiro

APPLICANT: TOKITOU, Funimo
 HIRATA, Takahiro

APPLICANT: TOKUSUMI, Tsuyoshi

APPLICANT: INOUE, Makoto

TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS

FILE REFERENCE: 50026-028001

CURRENT APPLICATION NUMBER: US/09/966,277

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: PCT/JP00/03195

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/283451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200739

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-277-63

Query Match 100% ; Score 10; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCACCC 10

Db 1 CTTTCACCC 10

RESULT 2-930-63

Sequence 63, Application US-09966930

Publication No. US20030022376A1

GENERAL INFORMATION:

APPLICANT: KITAAMOTO, Kai

APPLICANT: SHU, Tsugumine

APPLICANT: KUMA, Hidekazu

APPLICANT: OEDA, Yasuji

APPLICANT: ASAKAWA, Makoto

APPLICANT: HASOGAWA, Mamoru

APPLICANT: IIDA, Akiniro

APPLICANT: HIRATA, Takahiro

APPLICANT: INOUE, Makoto

TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

FILE REFERENCE: 50026/029001

CURRENT APPLICATION NUMBER: US-09/956,930

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: PCT/JP00/043194

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/203451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200740

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-63

Query Match 100.0%; Score 10; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 10; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

QY 1 CTTTCACCC 10

Db 1 CTTTCACCC 10

RESULT 3

Sequence 1, Application US-09823699

Patent No. US20020002143A1

GENERAL INFORMATION:

APPLICANT: Kano, Munehide

APPLICANT: Matano, Tetsuro

APPLICANT: Kato, Atsushi

APPLICANT: Nagai, Yoshiyuki

APPLICANT: Hasogawa, Mamoru

TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus

FILE REFERENCE: 50026/022002

CURRENT APPLICATION NUMBER: US-09/823,699

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 60/193,127

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: artificially synthesized sequence

US-09-823-699-1

Query Match 100.0%; Score 10; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 10; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

QY 1 CTTTCACCC 10

Db 1 CTTTCACCC 10

RESULT 4

Sequence 21, Application US-09972331

Patent No. US20020091083A1

GENERAL INFORMATION:

APPLICANT: KOMATSU, KIYOSHI

APPLICANT: HIGASHI, KIYOSHI

TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING

FILE REFERENCE: 7372/72170

CURRENT APPLICATION NUMBER: US-09/972,331

CURRENT FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: JP 2000/310624

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: DESIGNED OLIGONUCLEOTIDE PRIMER TO SYNTHESIZE

US-09-972-331-21

Query Match 100.0%; Score 10; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 10; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

QY 1 CTTTCACCC 10

Db 11 CTTTCACCC 2

RESULT 5

Sequence 43, Application US-09988115A

Publication No. US2003003747A1

GENERAL INFORMATION:

APPLICANT: Robl, James M.

APPLICANT: Goldsby, Richard A.

APPLICANT: Ferguson, Stacy E.

APPLICANT: Kuroiwa, Yoshima

APPLICANT: Tomizuka, Kazuma

APPLICANT: Ishida, Isao

TITLE OF INVENTION: Expression of Xenogenous (Human) Immunoglobulins in Cloned, Transgenic Ungulates

FILE REFERENCE: 50195/00803

CURRENT APPLICATION NUMBER: US-09/988,115A

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,625

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: US 60/256,458

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/714,185

PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: US 60/156,410

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 43

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
; US-09-988-115A-43

Query Match 100.0%; Score 10; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Title of Invention: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO: 11 CTTTCACCCCT 20

RESULT 6
US-09-966-277-43/C
; Sequence 43, Application US/09966277
; Patent No. US20020169306A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kai
; APPLICANT: SHU, Tsugumine
; APPLICANT: KUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Mamoru
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: TOKITOU, Fumino
; APPLICANT: HIRATA, Takahiro
; APPLICANT: TOKUSUMI, Tsuyoshi
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
; FILE REFERENCE: 50026/028001
; CURRENT APPLICATION NUMBER: US/09/966, 277
; CURRENT FILING DATE: 2001-09-27
; PRIORITY APPLICATION NUMBER: PCT/JP00/03195
; PRIORITY FILING DATE: 2000-05-18
; PRIORITY APPLICATION NUMBER: JP 2001/283451
; PRIORITY FILING DATE: 2001-09-18
; PRIORITY APPLICATION NUMBER: JP 11/200739
; PRIORITY FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 43
; LENGTH: 47
; TYPE: DNA
; ORGANISM: DNA
; FEATURE:
; OTHER INFORMATION: Artificial Sequence
; US-09-966-277-43

RESULT 7
US-09-966-277-44
; Sequence 44, Application US/09966277
; Patent No. US20020169306A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kai
; APPLICANT: SHU, Tsugumine
; APPLICANT: RUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: TOKITOU, Fumino
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
; FILE REFERENCE: 50026/029001
; CURRENT APPLICATION NUMBER: US/09/966, 930
; CURRENT FILING DATE: 2001-09-27
; PRIORITY APPLICATION NUMBER: PCT/JP00/03194
; PRIORITY FILING DATE: 2000-05-18
; PRIORITY APPLICATION NUMBER: JP 2001/283451
; PRIORITY FILING DATE: 2001-09-18
; PRIORITY APPLICATION NUMBER: JP 11/200740
; PRIORITY FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 43
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
; US-09-966-930-43

Query Match 100.0%; Score 10; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Title of Invention: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO: 1 CTTTCACCCCT 10

Db 13 CTTTCACCT 4

RESULT 9

US-09-966-930-44

Sequence 44, Application US/09966930

Publication No. US20030022376A1

GENERAL INFORMATION:

APPLICANT: KITAZATO, Kaito

APPLICANT: SHU, Tsugumine

APPLICANT: KUNI, Hidekazu

APPLICANT: UEDA, Yasuji

APPLICANT: ASAKAWA, Makoto

APPLICANT: HASEGAWA, Mamoru

APPLICANT: ITADA, Akihiro

APPLICANT: HIRATA, Takahiro

APPLICANT: INOUE, Makoto

TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

FILE REFERENCE: 50026/029001

CURRENT APPLICATION NUMBER: US/09/966, 930

CURRENT FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: PCT/JP00/03194

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/283451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200740

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-44

Query Match 100.0%; Score 10; DB 9; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 10

US-09-923-699-10

Sequence 10, Application US/09823699

Patent No. US2002002143A1

GENERAL INFORMATION:

APPLICANT: Kano, Munehide

APPLICANT: Matano, Tetsuro

APPLICANT: Kato, Atsushi

APPLICANT: Nagai, Yoshiyuki

APPLICANT: Hasegawa, Mamoru

TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus

TITLE OF INVENTION: Vector

FILE REFERENCE: 50026/022002

CURRENT APPLICATION NUMBER: US/09/923,699

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 60/193, 127

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 63

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: artificially synthesized sequence

US-09-923-699-10

Query Match 100.0%; Score 10; DB 9; Length 69;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 11

US-09-471-840-2

Sequence 2, Application US/09471840

Patent No. US20020081706A1

GENERAL INFORMATION:

APPLICANT: NAGAI, Yoshiyuki

APPLICANT: KATO, Atsushi

APPLICANT: MURAI, Fukashi

APPLICANT: ASAKAWA, Makoto

APPLICANT: SAKATA, Tsuneki

APPLICANT: HASEGAWA, Mamoru

APPLICANT: SHIODA, Tatsuo

TITLE OF INVENTION: Negative Strand RNA Viral Vector Having

FILE REFERENCE: 50026/004002

CURRENT APPLICATION NUMBER: US/09/471, 840

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: JP HEI 7-308315

EARLIER FILING DATE: 1995-10-31

EARLIER APPLICATION NUMBER: PCT/JP96/03068

EARLIER FILING DATE: 1996-10-22

EARLIER APPLICATION NUMBER: 09/070, 938

EARLIER FILING DATE: 1998-04-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 69

TYPE: DNA

ORGANISM: Human Immunodeficiency Virus

FEATURE:

NAME/KEY: variation

LOCATION: (35)..(35)

OTHER INFORMATION: v at 35 is a, c, or g, not t or u.

US-09-471-840-2

Query Match 100.0%; Score 10; DB 10; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 12

US-09-471-840-4

Sequence 4, Application US/09471840

Patent No. US20020081706A1

GENERAL INFORMATION:

APPLICANT: NAGAI, Yoshiyuki

APPLICANT: KATO, Atsushi

APPLICANT: MURAI, Fukashi

APPLICANT: ASAKAWA, Makoto

APPLICANT: SAKATA, Tsuneki

APPLICANT: HASEGAWA, Mamoru

APPLICANT: SHIODA, Tatsuo

TITLE OF INVENTION: Negative Strand RNA Viral Vector Having

FILE REFERENCE: 50026/004002

CURRENT APPLICATION NUMBER: US/09/471, 840

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: JP HEI 7-308315

EARLIER FILING DATE: 1995-10-31

EARLIER APPLICATION NUMBER: PCT/JP96/03068

; EARLIER FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 09/070, 938
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Chemical synthesis
; US-09-471-840-4

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCACCT 10
Db 16 CTTTCACCT 25

RESULT 13
US 09-728-207-2
; Sequence 2, Application US/09728207
; Patent No. US20020098576A1
; GENERAL INFORMATION:
; FILE REFERENCE: 50026/005001
; CURRENT APPLICATION NUMBER: US/09/728,207
; PRIORITY APPLICATION NUMBER: US/09/071,591
; PRIORITY FILING DATE: 1998-05-01
; PRIORITY APPLICATION NUMBER: JP HEI 7-285417
; PRIORITY FILING DATE: 1995-11-01
; PRIORITY APPLICATION NUMBER: PCT/JP96/03069
; PRIORITY FILING DATE: 1996-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (35)..(35)
; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.
; US-09-728-207-2

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCACCT 10
Db 17 CTTTCACCT 26

RESULT 14
US-09-728-207-4
; Sequence 4, Application US/09728207
; Patent No. US20020098576A1
; GENERAL INFORMATION:
; APPLICANT: NAGAI, Yoshiyuki
; APPLICANT: KATO, Atsushi
; APPLICANT: MURAI, Fukashi
; APPLICANT: SAKATA, Tsuneaki
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: SHIODA, Tatsuo
; TITLE OF INVENTION: Recombinant Sendai Virus
; CURRENT APPLICATION NUMBER: US/09/728,207
; PRIORITY APPLICATION NUMBER: US/09/071,591
; PRIORITY FILING DATE: 1998-05-01
; PRIORITY APPLICATION NUMBER: JP HEI 7-285417
; PRIORITY FILING DATE: 1995-11-01
; PRIORITY APPLICATION NUMBER: PCT/JP96/03069
; PRIORITY FILING DATE: 1996-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Chemical synthesis
; US-09-728-207-4

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCACCT 10
Db 16 CTTTCACCT 25

RESULT 15
US-09-070-938-2
; Sequence 2, Application US/09070938
; Patent No. US20020100066A1
; GENERAL INFORMATION:
; APPLICANT: Nagai, Yoshiyuki
; APPLICANT: Kato, Atsushi
; APPLICANT: Murai, Fukashi
; APPLICANT: Asakawa, Makoto
; APPLICANT: Sakata, Tsuneaki
; APPLICANT: Hasegawa, Mamoru
; APPLICANT: Shioda, Tatsuo
; TITLE OF INVENTION: Negative Strand RNA Viral
; TITLE OF INVENTION: Vector Having Autonomous Replication Capability
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,938
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-308315
; FILING DATE: 31-OCT-1995
; APPLICATION NUMBER: JP95/03068
; FILING DATE: 22-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T
; REGISTRATION NUMBER: 30,152
; REFERENCE/DOCKET NUMBER: 50026/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428 0200

TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0;
Constituents 0; Indels 0; Gaps 0;

QY 1 CTTTCACCC 10
||| | | | |
Db 17 CTTTCACCT 26

Search completed: March 19, 2003, 02:47:57
Job time : 51.5 secs

GenCore version 5.1.4.p5_4578
Copyright: (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

March 18, 2003, 23:53:50 ; Search time 1320.5 Seconds

(without alignments)
122.647 Million cell updates/sec

Title: US-09-702-498A-33
Perfect score: 10
Sequence: 1. CTTTCACCT 10

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listeing first 45 summaries

Database :

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1: EST:*
2: em_estba:*
3: em_esthm:*
4: em_estin:*
5: em_estmu:*
6: em_estov:*
7: em_estpl:*
8: em_hrc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
TA285H020	TA285H020
LOCUS	T. brucei sheared genomic DNA clone 285h02, reverse sequence, genomic survey sequence.
DEFINITION	28 bp DNA 13-DEC-2000
ACCESSION	AI485473
VERSION	AI485473.1
KEYWORDS	GI:11853036
SOURCE	GSS.
ORGANISM	Trypanosoma brucei.
REFERENCE	Trypanosoma brucei; Buglennozoa; Kinetoplastida; Trypanosomatidae;
AUTHORS	1 (bases 1 to 28)
COMMENT	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., El-Sayed,N., Hou,L., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrel@sanger.ac.uk and barrel@sanger.ac.uk
JOURNAL	Direct Submission

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	28 17	TA285H020
c 2	10	100.0	38 17	AJ485473 T. brucei
3	10	100.0	43 17	AJ332275 1M0606M011
c 4	10	100.0	67 17	AI75476 Arribalzaga
c 5	10	100.0	68 17	AZ805524
6	10	100.0	72 13	AZ805524 2M0066P02
				BE138421 x174904 x
				BE1783611 K135e05.y
				BE1783611 K135e05.y

Barrell, Oxford University Press, 1999).

Email: mlsavy@tgtr.org
 Details of *T. brucei* sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/projects/T-brucei/>.
 Location/Qualifiers

FEATURES
 source

1. 28
 /organism="Trypanosoma brucei"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="485h02"

BASE COUNT
 Query Match 100 0%; Score 10; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.8e-04;
 Matches 10; Conservative 0; Mismatches 0;
 Oy 1 CTTTACCCCT 10
 Db 9 CTTTCACCT 18

ORIGIN

RESULT 2

AZ332275/c

LOCUS AZ332275 38 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0060M1R Mouse 10kb Plasmid library Mus musculus genomic
 clone UGGC1M0060M1 R, DNA sequence.

ACCESSION A2332275

VERSION A2332275.1

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 38)

Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,' Islan,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: daunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0060 row: M column: 11
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 38.
 Location/qualifiers
 1. 38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGC1M0060M1"
 /clone_1ib="Mouse 10kb plasmid UGGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory. Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

BASE COUNT
 Query Match 100 0%; Score 10; DB 17; Length 38;
 Best Local Similarity 100.0%; Pred. No. 8.3e-04;
 Matches 10; Conservative 0; Mismatches 0;
 Oy 1 CTTTACCCCT 10
 Db 19 CTTTCACCT 10

ORIGIN

RESULT 3

AL754476

LOCUS AL754476 43 bp DNA linear GSS 17-JUN-2002
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-054E08-012357,
 genomic survey sequence.

ACCESSION AL754476

VERSION AL754476.1

KEYWORDS GSS

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE 1

Eukaryota; Vidiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosidae II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehever,P., Dekker,K., Saedler,H. and Weisshaar,B.

JOURNAL TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from *Arabidopsis thaliana* T-DNA transformed lines
 unpublished

REFERENCE 2
 AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
 JOURNAL TITLE A new *Arabidopsis thaliana* T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
 unpublished

REFERENCE 3

(bases 1 to 43)

COMMENT
 Ross, M., Li, Y., Strizhov, N. and Weisshaar, B.
 Direct Submission
 Submitted (17-JUN-2002) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linné-Weg 10, Kœln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g07160. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>

FEATURES
 Source

1. 43
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GR-03EB08-012357"
 /clone_1ib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pRP42 (g14732141gb AF123072.1), a copy number inducible derivative of pRFM1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

processed for submission. T-DNA derived sequences were removed, and selected for ampicillin resistance.

BASE COUNT 8 a
ORIGIN 10 c 8 g 17 t

BASE COUNT 23 a
ORIGIN 13 c 17 g 14 t

Query Match 100.0%; Score 10; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 33 CTTTCACCT 42

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

RESULT 4
A280524/c
LOCUS A280524
DEFINITION 2M005P22R Mouse 10kb plasmid UGGC1M library Mus musculus genomic
ACCESSION A280524
VERSION A280524.1 GI:12966335
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 67)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Dival,B., Hamil,C.,
Islam,H., Longcore,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederauern,A.,
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5006
Fax: 801 585 7777
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 Row: P Column: 22

Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 67.

FEATURES
Source
Location/Qualifiers

1. .67
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGC2M006P22"
/clone_id="Mouse 10kb plasmid UGGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotid kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (9147321141gbAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT 26 a
ORIGIN 8 c 22 g 12 t

BASE COUNT 23 a
ORIGIN 13 c 17 g 14 t

Query Match 100.0%; Score 10; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 57 CTTTCACCT 48

Query Match 100.0%; Score 10; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

Query Match 100.0%; Score 10; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
Db 34 CTTTCACCT 25

DEFINITION kh35e05.y1 Ascaris suum male head pamp1 v2 Chiapelli McCarter

ACCESSION AZ781553

ACCESSION AZ781553.1 GI:12914361

VERSION B7783611

VERSION B7783611.1 GI:15786503

KEYWORDS EST

SOURCE pig roundworm.

ORGANISM Ascaris suum

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris.

REFERENCE 1 (bases 1 to 72)

AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Isagardishvili,R., Ronko,I., Kennedy,S., Macquire,L., Beck,C., Underwood,K., Sephtoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wuston.wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of Pamp1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsp.h.edu) of the School of Public Hygiene and Public Health at Johns Hopkins University in Baltimore, MD. Seq primer: -40RE from Gibco

High quality sequence stop: 58.

FEATURES

source

1. 72 /organism="Ascaris suum"

/clone_id="Ascaris suum male head pamp1 v2 Chiapelli

McCarter"

/sex="Male"

/tissue_type="Head"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsp.h.edu) of the School of Public Hygiene and Public Health at Johns Hopkins University in Baltimore, MD."

BASE COUNT 10 a 22 c 15 g 25 t.

ORIGIN

RESULT 7

AZ781553

LOCUS AZ781553 72 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M021I3F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLC2M021I03 F, DNA sequence.

Query Match 100.0%; Score 10; DB 13; Length 72;

Best Local Similarity 100.0%; Pred. No. 9.5e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10

Db 26 CTTTCACCT 35

RESULT 8

B36161/C

LOCUS B36161 73 bp DNA linear GSS 17-Oct-1997

DEFINITION HS1038-Al-E11-MF.ab1 CIR Human Genomic Sperm Library C Homo sapiens genomic clone Plate=Cr 820 Col=21 Row=1, DNA sequence.

Query Match 100.0%; Score 10; DB 17; Length 72;

Best Local Similarity 100.0%; Pred. No. 9.5e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10

Db 34 CTTTCACCT 43

BASE COUNT 5 a 26 c 3 g 38 t.

ORIGIN

RESULT 11
 BH405910
 LOCUS BH405910 88 bp DNA linear GSS 19-APR-2002
 DEFINITION RPCI-23-105F8 SP6E RPCI-23 Mus musculus genomic clone RPCI-23-105F8
 , DNA sequence.
 ACCESSION BH405910
 VERSION BH405910.1 GI:17460796
 KEYWORDS GSS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 93)
 REFERENCE 1 (bases 1 to 88)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 , M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid insets
 COMMENT Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah, Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: odunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0537 row: H column: 21
 Seq primer: CGTTGTTAAAGGCGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 93.
 FEATURES source
 Location/Qualifiers
 1. .88
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-105F8"
 /clone_id="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 19 a 34 c 11 g 24 t
 ORIGIN 100.0% Score 10; DB 17; Length 88;
 Query Match Best Local Similarity 100.0%; Pred. No. 9.9e-04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTCACCT 10
 Db 77 CTTTCACCT 86

RESULT 12
 AZ659766
 LOCUS AZ659766 93 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M0537H21F Mouse 10kb Plasmid UGCLM library Mus musculus genomic
 clone UGCLM0537H21 F, DNA sequence.
 ACCESSION AZ659766
 VERSION AZ659766.1 GI:1796912
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 93)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 , M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid insets
 COMMENT Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah, Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: odunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0537 row: H column: 21
 Seq primer: CGTTGTTAAAGGCGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 93.
 FEATURES source
 Location/Qualifiers
 1. .93
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0537H21"
 /clone_id="Mouse 10kb plasmid UGCLM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, *T*1-resistant, F"
 /note="Vector: pWpL2nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www-jax.org/resources/documents/dnars/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotid kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (g141321141gb(AF120721)), a copy-number
 indelible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance." (Stratagene) cells
 BASE COUNT 17 a 30 c 20 g 26 t
 ORIGIN 100.0% Score 10; DB 17; Length 93;
 Query Match Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTCACCT 10
 Db 9 CTTTCACCT 18

RESULT 13
 AG101870
 LOCUS AG101870 93 bp DNA linear GSS 03-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.
 ACCESSION AG101870
 VERSION AG101870.1 GI:16722387
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_id:PTB Chimpanzee Male
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;

		source
REFERENCE		1. -97
AUTHORS		/organism="Homo sapiens"
Fujiyama,A., Hattori,M., Toyota,A., Taylor,T.D., Yada,T.,		/db_xref="taxon:9606"
Totoki,Y., Watanabe,H. and Sakai,Y.		/clone="IMAGE:1861992"
TITLE		/clone_id="NCI_CGAP_OV26"
JOURNAL		/sex="female,"
COMMENT		/tissue_type="papillary serous carcinoma"
AUTHORS		/dev_stage="adult"
Fujiyama,A., Hattori,M., Toyota,A., Taylor,T.D., Yada,T.,		/lab_host="DH10B"
Totoki,Y., Watanabe,H. and Sakai,Y.		/note="Organ: Ovary; Vector: pAMP1; mRNA made from papillary serous ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22, Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimberes@gsc.riken.go.jp; URL: http://hgp.gsc.riken.go.jp/ Tel:81-45-503-9111; Fax:81-45-503-9170)		Clones from the chimpanzee BAC library PTB (this BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS		
Sequencing: M13Rev		
LIBRARY		
Vector : pKS145		
R_Site 1 : SacI		
R_Site 2 : SacI.		
FEATURES		
source		
1. -93		
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/clone="PTB-105A3.R"		
/sex="male"		
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ORIGIN		
Query Match		
Best Local Similarity 100.0%; Score 10; DB 17; Length 97;		
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Pred. No. 1e+05; 0; Indels 0; Gaps 0;		
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 CTTTCACCT 10		
Db 45 CTTTCACCT 54		
RESULT 14		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053527	
mRNA sequence.	A1053527	
VERSION	A1053527.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 15		
A1053527		
LOCUS	A1053527	
DEFINITION	A1053527	
mRNA sequence.	A1053527	
VERSION	A1053527.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 16		
A1053527		
LOCUS	A1053527	
DEFINITION	A1053527	
mRNA sequence.	A1053527	
VERSION	A1053527.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 17		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 18		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 19		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 20		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 21		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 22		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 23		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 24		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 25		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 26		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 27		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 28		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 29		
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LOCUS	A1053521	
DEFINITION	A1053521	
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VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 30		
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LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 31		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 32		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 33		
A1053521		
LOCUS	A1053521	
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mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 34		
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LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 35		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 36		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 37		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 38		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 39		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 40		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 41		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 42		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 43		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 44		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 45		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 46		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 47		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 48		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 49		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 50		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 51		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 52		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 53		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 54		
A1053521		
LOCUS	A1053521	
DEFINITION	A1053521	
mRNA sequence.	A1053521	
VERSION	A1053521.1	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
COMMENT		
RESULT 55		
A1053521		
LOCUS	A1053521	

Best Local Similarity 100.0%; Prcd. No. 1e+05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCACCT 10
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Db 31 CTTTCACCT 40

Search completed: March 19, 2003, 01:24:57
Job time : 1328.5 secs